



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 204048**

**TO: Ruixiang Li**  
**Location: rem/4D75/4C70**  
**Art Unit: 1646**  
**Friday, October 13, 2006**  
**Case Serial Number: 10/668767**

**From: Dwayne Hill**  
**Location: Biotech-Chem Library**  
**REM-1A41**  
**Phone: (571)272-8972**

**Dwayne.Hill@uspto.gov**

### **Search Notes**

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Dwayne Hill  
STIC Biotech/Chem Library  
(571)272-1972

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78733

10-324

204048

114

## STIC-Biotech/ChemLib

From: Li, Ruixiang  
Sent: Friday, October 06, 2006 11:40 AM  
To: CRFF STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/668,767

Please do a standard search on:

aa 5128

- (i). SEQ ID NO: 128 against interference amino acid databases;  
(ii). SEQ ID NO: 127 and ~~128~~ against interference nucleic acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

127 na 15387

Seq ID 127 1-5000

Em ☒Leg ☒

ME  
\*\*\*\*\*  
Searcher: 10/6  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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**Li, Ruixiang**

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**From:** Hill, Dwayne (ASRC)  
**Sent:** Tuesday, October 24, 2006 1:52 PM  
**To:** Li, Ruixiang  
**Subject:** Sequence Search Results for 10/668767 Seq. ID 128 (1-1700)

Dear Examiner,

I just checked SCORE and the results for your sequence search are there now.

\*\*\*\*\*

<http://es/ScoreAccessWeb/GetItems.action?ApplId=10668767&ItemType=4&VersionNo=10>

After downloading files, use **Microsoft Word** to view, manipulate and print.

\*\*\*\*\*

If you have any problems, please do not hesitate to call me for assistance.

Please let me know if you have any questions. Thank you for using STIC services.

Dwayne Hill  
STIC/Biotech Library  
REM1A64  
X28972



search  
feedback form.d

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2006, 23:32:44 ; Search time 87 Seconds  
(without alignments)  
5159.277 Million cell updates/sec

Title: US-10-668-767-128

Perfect score: 26800

Sequence: 1 MAEAGGAGSEQDDVFLRTE.....WDFPFGVGCFRKQYEDLMGE 5128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11887.5	44.4	4968	2	US-09-424-783-5
2	11386.5	42.5	4872	2	US-09-424-783-3
3	11349	42.3	5037	2	US-09-424-783-4
4	11325.5	42.3	5032	2	US-09-538-092-979
5	11295.5	42.1	4866	2	US-09-424-783-2
6	658	2.5	2749	2	US-09-385-222A-4
7	654	2.4	2713	5	PCT-US96-01735-1
8	336.5	1.3	240	1	US-08-114-555A-8
9	336.5	1.3	240	2	US-08-559-397A-14
10	334.5	1.2	240	1	US-08-114-555A-6
11	334.5	1.2	240	2	US-08-559-397A-12
12	313.5	1.2	2262	2	US-09-949-016-8849
13	308	1.1	3259	2	US-09-949-016-6507
14	305.5	1.1	5024	2	US-09-710-279-2964
15	305	1.1	2733	2	US-09-949-016-11433
16	303.5	1.1	10182	2	US-09-134-001C-3159
17	302	1.1	3878	2	US-09-914-259-11
18	288	1.1	3248	1	US-08-353-700-1
19	288	1.1	3248	5	PCT-US95-16216-1
20	285	1.1	3210	2	US-09-538-092-1154
21	276.5	1.0	2854	2	US-09-150-867-1
22	276.5	1.0	2954	3	US-09-724-584-1
23	263	1.0	200	2	US-10-104-047-3679
24	259.5	1.0	2349	2	US-09-538-092-914
25	255.5	1.0	3433	2	US-09-538-092-1136
26	249.5	0.9	2482	1	US-08-328-254-6

ALIGNMENTS

RESULT 1

US-09-424-783-5  
; Sequence 5, Application US/09424783  
; Patent No. 6780608

GENERAL INFORMATION:

; APPLICANT: Hakamata, Yasuhiro  
; APPLICANT: Nishimura, Seichiro  
; APPLICANT: Barsoumian, Edward Leon  
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein  
; TITLE OF INVENTION: and DNA Molecules Coding Therefor  
; FILE REFERENCE: 0652.2000000  
; CURRENT APPLICATION NUMBER: US/09/424, 783  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/02926  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: DE 197 22 317.6  
; PRIOR FILING DATE: 1997-05-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 4968  
; TYPE: PRT  
; ORGANISM: Oryctolagus cuniculus  
; US-09-424-783-5

Query Match 44.4%; Score 11887.5; DB 2; Length 4968;

Best Local Similarity 46.7%; Pred. No. 0;

Matches 2459; Conservative 903; Mismatches 1455; Indels 451; Gaps 92;

QY	4	AEGGASEQDDVSFLRTEDMVLCSLTAT---GERVCLAAEGFGNRHCFLENIAD-KNIIPP	58
DB	2	ADGGE-DEIQFLRTDDEVVLQCTATTHKQKCLAAEGFGNRLCFLESTNSKNVPP	60
QY	59	DLSCQVFIEQALSVRALQELVTAAGSETGK-----TCSGHRITLLYGNAI	104
DB	61	DLISCTFVLEQSLVRALQEL-ANTVEKSEGVQDVVEKMKFMKTAQGGHRTLLYGHAI	119
QY	105	LLRLHNSDMLACI-LSTS--SSODKLAFLDVLQOHSQGEACWMTLHPASKQRSEGEKVRVD	163
DB	120	LLRHYSQGMVLCCLSTSRSSDTKLAFDVLQEDDTGEACWMTIHPASKQRSEGEKVRVD	179
QY	164	DLILVSVATERLYLHTTKNEVSVINASPHVTHWSVQPYGTGISRKKYVGVYFGDVLRF	223
DB	180	DLILVSVSSRYLHLSYNGSLHVDAAFPQTLWSVPATISSGSEAAQ--GYLIGDVLRL	237
QY	224	HGG-DECLTIPSTWTGCGQNVVYEGGSVMSQARSLRLEARTKWAGGTINWHPRI	282
DB	238	HGHMDECLTVPSEGBGEQRRTVHVGAGSVHARSRLRLETLRVANSQSHIRWGQPR	297



Db 2275 QSCQMLVSGXPDIQWNPVEGERYLDLFLRFAVFCNGESVEBNANVVVRELLIRREPCFGPA 2334  
Qy 2457 LRGE-GEGLKAI V DANKWMSRIADRRKLRMEQEGDVFNSHLPES-----DEDE 2506  
Db 2335 LRGEQGNLLAMEBAIKAE-----DPSRQSPSTSGSKTLDTBEED 2379  
Qy 2507 DYIDTGAAILNPFYCTVLDLGRCAPDAGVIALGKNESIRARAILRSVLPLEDLQGVLSLR 2566  
Db 2380 DTIHMGNAIMFYAALIDLLGRCAPEMHLIHAGKEAIRSILKSLPLDGLGVVISIA 2439  
Qy 2567 FTLLNPAAGEBERPKDMSGLIPGHQSVGLFLERVYGIETQBELFYKLEBAFLPDLRAA 2626  
Db 2440 FQMPTIAKQGNVPEDMGAGCPDHKAAMVFLDRVYGIQDFLHLLHVGFLPDLRAA 2499  
Qy 2627 TMLDRNDCESDMALSMRYTGNSTPLILLIKHAYPNEAENYASILLDTATHTVYRLSKR 2686  
Db 2500 ASLDTAALSATDMALANRYCTAVPLTRCAPLFACTEHHASLIDSLLHTVYRLSKG 2559  
Qy 2687 MLTKQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLTLHYERCAK 2746  
Db 2560 SLTKAQRDSIEVCLLSICQLRPPSMQHLRLRFLVDPVLLNEHAKMPLKLLTNHYERCWK 2619  
Qy 2747 YYGSTGAGGAFGASDEKRLTMMFLPSNIFDSLSKMDYBELFKALPCLIAIGCALPP 2806  
Db 2620 YYCLPG-GWGNFGAASEBELHLSRKLFWGIFDALSKKYEQLFKALPCLISAVAGALPP 2678  
Qy 2807 DYSLSKNYDDPEYKGEQAAGLDNDPOYDPOPTSSVALNNDLNTIVOKFSEHYHDWAS 2866  
Db 2679 DY-MESNVYSWM--BKQSSMSSEG-NFNPQPVDTSNIIIPKLEYFINKYAEHSHDKWSM 2734  
Qy 2867 RKIENGWYVGEWSQKTHPRKLPKYNMLNDYKERYKEPVRESILKALLAIGWSVEHSEV 2926  
Db 2735 DKLANGWYGEIYSDSKIQPLMKPYKLLSEKEIYRWPIKESKTMLANGWRIERT- 2793  
Qy 2927 DIPSNRSMRRQSKGGRPEIVTDSATPDYNPDPVDMNTLTLRSRQWMAERLADNA 2986  
Db 2794 ---EGDSMALVNRTRRISQTSQVSDAA--HGYSPRADMSNVTLRSRDLHAMAENMAENY 2848  
Qy 2987 HDIWAKKKEELVTNGGIHPOLVBYDILLTKKEKKQDERQSEFLKYLOYGYKLHRPSK 3046  
Db 2849 HNIWAKKKLESGGGGNHPLLVYDYLTAKEKAKREKAQDILKFLQINGYAVSRGFK 2908  
Qy 3047 APOSTEQTTGVALELFAFVSLLEKLIQYIDRATINMKLLKPSFTFSRRRSFKTSTRDI 3106  
Db 2909 DLELDT-----SIEKFAFVFLQQLRYVDEA--HQYILEFDGGSKSGEHPYEGEI 2960  
Qy 3107 RFFSKAVLPLMEKYFSTHRNFIYAVAT-ATNNVGAASLKEKEMVAALPCKLASLSRLA 3165  
Db 2961 KFFAKVVLPLIDQYFKNHRLYFLSAASRPLCSGGHASNKEKEMVTSLFCKLGLVVRHRIS 3020  
Qy 3166 APGPVRI TVRCLQVLVKGIDAKSLVKNCPPEPIRTSMITFPNNVADDVGHITMLODKY 3225  
Db 3021 LFGNDATSI VNLCHTIGQTDARTVMKTKGLESVKSAFLADNAEDELKTMENLKQGF 3080  
Qy 3226 AHLRGTHLKTSLGVINGVLLPIITAKFDHLANCEYGAIDLLEIDRIVASVYKMLGSLVAL 3285  
Db 3081 THTRNQPRGVQIINVTYVALLPMLSSUFEHIGQHOFGEDELLIEDVQSVCRILSLVAL 3140  
Qy 3286 GTDASLTHDRKYLKTEIERHKHPALGSCLGAFSTFPFVAFLEPHLNKRNQFSLNRIADHS 3345  
Db 3141 GTSKSI-----YVERQSRALGCLAAAFAGAFVAFLETHLNKNIYSYNTKSSRE 3191  
Qy 3346 LEAQIDIMQKOE-C--MPTLETILGEVQFVBSDKTYNEAPHIIDVPLICSYLPFWFA 3402  
Db 3192 RAALSIPANVEDVCPNIPLSEKLMBEIVELAESGIRYTMQPMHMEVILPMLCSYMSRWWE 3251  
Qy 3403 QCPDNVPTGGNHVTWTAHNNOLLKNVLKLIKNIENAPWTRATVYQQIIINS 3462  
Db 3252 HGPENPGRAENCCCTALNSENWTLGNLTKLIYNNLIGDEGAWKRLAVFSQPIINKVK 3311  
Qy 3463 BELLRDSFLPLAERVKRTRDNNMFHEESLRGFIKSDTSDTSQVESQIQEDMOLLVRDIYS 3522  
Db 3312 POLLKTHFLPLMEKUKKKAAMVVSBEHLKA---EARGDMSEALLILDEFTTLARDLYA 3368

Qy 3523 FYPLLIKYVDLQRNHWLNRNVPEAEELYNHVAEIFNIWKSQYFLKEBQNFISANEIDNM 3582  
Db 3369 FYPLLIREFVDYNRAKWLKEPTPEAEELFRMAEVLFWYKSHNPKREBQNFVQNEINNM 3428  
Qy 3583 VLIMPTATRRVT--AVTDGTPQGGGKKKKHRRDKRDXEVOASLMAVACLKRLPLVGLN 3640  
Db 3429 SFLITDTTKSMKSAASD-----QERKMKRKGDR--YSMTQSTSLIIVAAKRLPLIPLN 3479  
Qy 3641 LFAGREOELVQHCKDRFLKMWSEODVAEFAKTJLTLPDKI--DPADEMSWQHYLSKLSGSK 3699  
Db 3480 ICAPGDELALAKNRSFKDTEDEVDRDIIRNNIHLQCKLEDPA--IRWQWALY-----K 3532  
Qy 3700 SKSNITVETAKNAKIIDDTVERIVAMSKVLFGI-----HMIDHPQMSKNVY 3747  
Db 3533 DLPNRTEETSDP-----EKTVERVLDIANVLFHLEQSKPIGRRYVNLVEHPQRSKAVM 3587  
Qy 3748 RSVVISIQRKRAVIACFQRTSLHSLPRHACNI PARTIYELWLE--EENIGQEWMLDITQS 3806  
Db 3588 HKLLSKQRKRAVACFRMAPLYNLPRAVNLFLQGYEKSWIETEEHYFEDKLIEDLAK- 3646  
Qy 3807 FEDAEALKSDVVEBEGEKDPDLTOLVTTFCRGAMTERSQAQEDPLYMSYAHIIAKSCGEE 3866  
Db 3647 -PGAEPPEED--EVTKRVDPHLQHILLFSRTALTEKC--KUEEDFLYIAYADIAMAKSCHDE 3702  
Qy 3867 EEEGGESEEGGEAEAEDEGRASIHQEQEMEKQKLLFHQARLADRGVAEMVLLHISASKG 3926  
Db 3703 EDDDGEEBVK-----SFEKEMEKQKLLYQARLHARGAAEMVLQTIASKG 3749  
Qy 3927 LPSBMWKTTLQLGISILRGNDIOMQMLNHLKDKKDVGPPTSIAGLMNSCSVLDLDAFE 3986  
Db 3750 ETGPMVAATLKLGAAILNGGNSVTQKMLDYLKEKDVGPFOQSLAGLQMSVLDLNAFE 3809  
Qy 3987 RNTYAEGLGVGLEGAAGEKNMHDAEFTCALPRFTQLTCEGNLDMQNYLRTQAGNTTVN 4046  
Db 3810 RQNAEGLGMVTEGSGEKVLQDDFEFTCDLFRFQLLCEGHNSQFNVLRQTQGNNTTVN 3869  
Qy 4047 VVICTVDYLLRLOSIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNLTITEYIQGPCT 4106  
Db 3870 IIIITVDYLLRVOSESISDFYWYSGKVIDBQGNFNSKAIQVAKQVFNLTITEYIQGPCT 3929  
Qy 4107 QNOQALSHRSLWDVAVGGFLFLFSHQDKLSKHSQVOLLKELLNLOKDMI PMMLSMLEGN 4166  
Db 3930 GNQOQSLAHSRLWDVAVGFLHVFAHQMKLSQDSQSIELLKELMDLQKDMVYVMLLSMLEGN 3989  
Qy 4167 VVNGTIGKQWDTIVASASVVELILKYFDMFLKLDLTSSASFOEIDANNQWVLPKDPK 4226  
Db 3990 VVNGTIGKQWDMVLVESNNVEMTLKFDMPFLKLDLTSSDTFKBEDDGDGKIISKRDHF 4049  
Qy 4227 EKMEQOQSYTPETIEFLACCETNHDGKLDYIGCDFRHEPAKEIGFNLA VLLTNLSSEHM 4286  
Db 4050 KAMESHKHYTOSETFELLSCAETDENETLDYEEFVKRHEPAKDIGFNVA VLLTNLSSEHM 4109  
Qy 4287 PNEPLARLEFETAGSVLNYFEPFLGRIEIMGSKRIERVYFEIKESNTEQWKEKPOIKESK 4346  
Db 4110 PNETRLQTFLEAESVLNYFOPFLGRIEIMGSAKRIERVYFEISESSRTQWEKPOIKESK 4169  
Qy 4347 RAFPYSIVTEGGDEKLEAFVNFCEDAIFEMTHASGLMAASEESVG--GTKNREASVYMWG 4405  
Db 4170 RQFIDVWVEGGEKEMELFVNFCEDTIFENQLAAQI---SESDLNKSANKERSEK --- 4223  
Qy 4406 DDDDERAGKDPF-----RRGLQSVKQGVATAFSSLSPSNIAKAKIADNQWPPPAELAVGF 4459  
Db 4224 ERPEQGPQGGFVSFVLRVSALPAIRNYLTLRMLSLKSLLKQKMKKMTVKDMVTAF 4283  
Qy 4460 FPMFIFYLPYLYGVVVRVYIFGVLLGLMRGPQTDPPP-----PEPTEEBKI 4507  
Db 4284 FSSYSIFMTLLHFVASVFRGFRIVCSLLGGSLVEGAKKIKVAELIANMPDPTQDEVR 4343  
Qy 4508 QQ---LHRLLATQSSSHLPALPADDTGQMVSAFGLDITKEDNGQIQVKPHESPSTS 4563  
Db 4344 GDGEGEGRKMETTLPSEDLTDLKELTSESLLSDIFGLDL-KRGGQYKLIPIH----- 4396



Qy 1129 WAPGYNEEKYSGNTESFGKQWAVGVGVFLDLIDKTTISFSLNGELLMDALGETTFA 1188  
Db 1121 LCLKAAG-ASVGTKVGVILGVPMQPGDVGVMGINLDASIMFTLNGELLITNKGSLELAF 1179  
Qy 1189 DVQGDN-FVPACTLGVGQKARLITYGQDNTLYKYTTTCGLQEGYEPFCVNMKRDVTHYTK 1247  
Db 1180 DYEIENGFPVPCISGLSIGRMNLTGDTASTFKFTYTCGLQEGYEPFAVNMNRDVMWFSK 1239  
Qy 1248 DQIFENTDEMIDTRIDVTRIPAGSDTPCLIKISHNTFETM-EKANWEFLRLSLPVICHN 1306  
Db 1240 RLPTFVNVPK-DPHIEVVRIDGTMDSPCLKVTHKTFGTQNSNANYICLSNPVCHS 1298  
Qy 1307 EFIDEAEKARWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNOEEL 1366  
Db 1299 SF----- 1300  
Qy 1367 PSSQKRLPSRPPRKGSWTRGVTTQNNYLNLOPQGVNGHIRSTEABEMAKYDLGAQGLTPD 1426  
Db 1301 ----- 1300  
Qy 1427 DKDKRGSRPFKFRSKGESSDRAKSRKSTPDPFSDTEVS PERGARRPNPQIKVSOAN 1486  
Db 1301 -----SHSPCLDSEA----- 1310  
Qy 1487 QRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSAETETVGEIIFDAECLKLI 1546  
Db 1311 -----FOKEKQM-QEILSHTT-----QC----- 1328  
Qy 1547 NEYFYGVRIYQGPQTHYVIGWVTTQVHLHSDKRNQSKVTSSVITDDYDRVVENNRQ 1606  
Db 1329 ---FYSIRIFAGQDPCSVWGVMTPDVHLYSEKFDLNKCTVTVTLGDERGRVHESVKRS 1385  
Qy 1607 SCYVRADELYNEVMAEATAKAGSQMGFICGSDTSGVSFTCEGKDTSKFKWEPETK 1666  
Db 1386 NCYMWVGDDV---VASSQSRSSRVNDLEIGCLDLAMGMLSFSANGKELGTCYQVEPNTK 1442  
Qy 1667 LPPAIFVEATSEKILQIELGRSATSLPLSAAVLPTSDKHVTPQPPRLKVQCLKPHOWAR 1726  
Db 1443 VPPAVFLOPTSTSLFQFELGKLKXAMPLSAAIFKSEENPVQCPPLDLVQTIQPVLSR 1502  
Qy 1727 VPNSLOVHALKSLDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLSLFSHTL 1786  
Db 1503 MENSFLKVETERVSRHGVVQCLEPLQWMLHIPEENRCVDILELCEQEDLMQFVHTL 1562  
Qy 1787 TLYAALCVQSNVRAAHALCTHVQKOLLYATQSYMSGPIRQGFVDLLIALHLSHATTM 1846  
Db 1563 RLYSAVCALGNSRVAYALCSHVDLSQLFHAIDNKYLPGLLRSGFYDILLIHLANAKERK 1622  
Qy 1847 EACKNEFVPLGPPELK--ALYEEDPMGHSLSRLOTES--VRQMKWTDIAESIT-EISNLY 1902  
Db 1623 LMKNEYIIPITSTTRNIRLVPDESCKHGLPGVGPRTCLKFGFKFSTPCFVVTNEERQKQ 1682  
Qy 1903 SPYFPLEVAREBFVMOALAEAVETNOVHNRDPVGGSNENLFLPLIKLVDRLLLVGMRRD 1962  
Db 1683 SPEPLELILMKALSMLTEAVQCSAHIRDPVGGSVFQFVPLKLVGTLLVMGVFCDD 1742  
Qy 1963 VEKLLIMNTPETW-DPSFD-KEGKDEHR-----KGLLHMK 1995  
Db 1743 VRQILLDLDPVSFVGHSDADTBEGAEBEVSQVEEKAVERAGEKTSKEARKEAPVRGLLQTR 1802  
Qy 1996 MAEGKALQWVYLQHLNDIOLRHRVEALIAFAHDPVGLDQDOLRRYTEIKOS-DLPSAV 2054  
Db 1803 LPESVKLOCELLSLVCDCELOHVEALVAFGDIIYVKLQANQKFRYNELMQALNWSAAL 1862  
Qy 2055 AAKTRERFCPPREQONAILSPKHLNEEDKENCPCGEBELIARMNEFHTLMAHVSLLHALQ 2114  
Db 1863 TARKTRERFPPQEQINMLNF-----QLGENCPCPEIREELYDFHEDLLVHCVG----- 1913  
Qy 2115 EPDAAENGEPEAKGAFGLKYNINVTKELEBEAKAIEBPKPTPEEK-----FRKVL 2167  
Db 1914 --PLEEEEBEEDTSWTGKRLTVYKI-----KGPPKPEKEQPTEEBERCPTTLKELI 1964  
Qy 2168 IQTIVNWAEESQIETPKLVRENFSLLRQYDAVAGELIRALEKTYVINAKTLKDVAEMVVG 2227

Db 1965 SOTMIRWAQSDQODAEVLVMMFNLRROQYDSIGELLQARUKYTTISHASVSDTINLAA 2024  
Qy 2228 LSOIRALLPVQMSQEEBELMRKELWKLNNHHTFQHPDLIRVLRLVRNVMVMMNTLGR 2287  
Db 2025 LQIRSLLSVRMGREBELLMINGLDIMNNKVYQHPENLRVLGMHETVMEVVMVLG-- 2082  
Qy 2288 AQAQSDAQSSQVPAEDSEKEDTSHEMVAVACCRFLCYFCRTGRQONQKAMDFHDFLLENS 2347  
Db 2083 -----TEKSQIAFPKMWASCCRFLCYFCRISRQONQKAMEHLSYLENS 2126  
Qy 2348 NILLSRPSLRGSTPLDVAYSLSMTELALAEHYLEKIAVLSRGLQSNSELVKGY 2407  
Db 2127 SVGLASPMRSGSTPLDVAASSVMNNELALGLEBEPDLEKRVVTVYLAGCGLSCPMLLAKGY 2186  
Qy 2408 PDLGWDPVEGERYDLDFRFCVWVNGSVSEENANLIVRLIRRRPECLGPALRGE-GEGLLK 2466  
Db 2187 PDVGNPIEGERYLSFLRFVAVFVNSEVENASVVVKLLIRRRPECFPALRGEKGGLLA 2246  
Qy 2467 AIVDANKMSERIAARRKRLREMEQGVNFSHPLE-SDEDEDYIDTGAALINFYCTLVDL 2525  
Db 2247 AMQGAIKISSPA-----LDLPQSG---YKREVPEDGEEBEEIVHMGNAIMSFYSALIDL 2298  
Qy 2526 LGRCAPDAGVIALGKNESLRARAILRSLVPLEDLOGVLRLFTLNLPAAAGEERPKS--DM 2583  
Db 2299 LGRCAPEMHIQTKGEAIRSILRSLVPTEDLVGIISPLKL--PSLNKDGSGSVSPDM 2356  
Qy 2584 PSGILPGHKOSVGLFTEERVYGIETOELFYKLEAEFLPDLRAATMLDRNDRCESDMALSM 2643  
Db 2357 AANFCPDHKAAMPWLFDRVYGIKQOTPLHLHLEVGLPDLRASASLTVALSTTESALAL 2416  
Qy 2644 NRYIGNSILPLLKHAYFYNEAENYASLLDATALHTVYRLSKNRMJTKQREAVSDFLVAL 2703  
Db 2417 NRYICSAVPLLTRCAFLPFAGTEHYTSLIDSTLQTVYRLSKGRSLTKAQRDTIECLLAI 2476  
Qy 2704 TSAMQPSMLKLRLKTLVDVSKLSEYTTVALRLTLHYERCAYKYGSGTAGCQAGFAGSSD 2763  
Db 2477 CNHLRPSMLQQLRLRVDFVQPLNDYCKMPLKLLTNHFEQCKWY-CLPSGWSGYGLAVE 2535  
Qy 2764 EEKRLTWMLFSNTFDSLSKMDYBEPFLGKALPCIIAIGCALPPDY-----SLSKNYDD 2816  
Db 2536 EELHLEKLPWGFIDSLSHKKYDPLFRMSLPCUSALAGALPPDYDLTRITATLEK---- 2591  
Qy 2817 EFGYKEAAGDLONPQDPQOPINTSSVALNNDLNTIVQKFESEHYHDAAWASKIENGWYVG 2876  
Db 2592 -----QVSDVADG-NEDPREINTINFSLPEKLEVIYTKVAESHSHDWACEKSGWKYG 2644  
Qy 2877 EGWSDSQKTHPRLPKYNMLNDYKERYKEPVRESLKALLAIGWSVEHSE-----VDIPSN 2931  
Db 2645 ISLDENVKTHPLIRPPFKTLTEKEKEIYRWPAFRESLKTMLAVGWTVERTKEGEALVQLREN 2704  
Qy 2932 NRSSMRQSKSGRPPPEIVTDSATPPDYNHPVDMTNLTLSREMNMAERLADNAHDIAWA 2991  
Db 2705 EKLRSVSQTSQGN-----SYNPAPLDLSNVVLSRELOQGVVEVVAENVHNIWA 2751  
Qy 2992 KKKKEELVTNGGGTHPOLVPYDLTLTKKKKDRERSQEFKLYQYQGYKLRHPSKAPQSD 3051  
Db 2752 KKKKLELESKGGSHPLVPYDTLTAKKFDREKAQDLFKFLQVNGVIVSRGMKMD 2811  
Qy 3052 TEQTTTGVAIELRPAYSLLEKLIQYIDRATINMKLLKPSSTTFSRRSSPKTSTRDKIFPSK 3111  
Db 2812 -----AFSMEKRFAYFKKILKYVDSAQEFIAHLE-AIVSSGKTEKSPHDQEIKFFAK 2864  
Qy 3112 AVLPLMEKYFSTHRNYFI-AVATATNVNVAASLEKEMVAALFCKLASLLRSRLAAGPD 3170  
Db 2865 VLLPLVDQYFTNRLYFLSSPLKPLSSSGYASHKEMVASLFCCKLAALVRHRLSLFGSD 2924  
Qy 3171 VRITVRCIQLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQOGKYAHLRG 3230  
Db 2925 STTWVSCULHIAQDLTRTNVMSSELVKAGLRAFFESAEDLEKTSNLKLGKTHSR- 2983  
Qy 3231 THLK--TSTSLGYINGVLLPILTAKFDFHLANCEYGADELLDIBIQVASYKMLGSLYALGTDA 3289



Db 2984 TQIKGVSONITYTTVALLPILTSIFEHVAHQFGVLLLDGVQVISCVRILCSLYSLGTGK 3043  
Qy 3290 SLTHDRKYLTEIBRHKPALGSCIGAFSSFPVAFLEPHLNKQFSLNRIADHS--L 3346  
Db 3044 NI-----YERQRPALGECIASAAIPVAFLEPTLNRNALSVFNTKTPRERSIL 3094  
Qy 3347 EAQDIMKQBQCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLLCYSLPFWAAGPD 3406  
Db 3095 GMPDTVEEMCPDIPQLEGLMKEINDLAESGARYTEMPHVIIEVILPMLCNVLSYMWERGPE 3154  
Qy 3407 NVPTTGNHVTMTVAEHNOLLKNVLKLIKKNIGNENAPMWTIATYTOQIINSSEELL 3466  
Db 3155 NLSPTGCCSKVTSEHLSLILGNILKIIINNLIIDEASWMKRIAVVAQPIISKARPDLL 3214  
Qy 3467 RDSPLPLAERVKRTDNMFKEESLRGFIKSSDDTTSQVESQIQEDWQLLAVRDIYSFYL 3526  
Db 3215 RSHFIPTLEKXKKAIVTQVEEOLKA---DGKGDTOEABELLIDEPAILCRDLAYFPM 3271  
Qy 3527 LIKYVDLQRNHLNRNNVPEABELYNHVAEINFNIWSKSOYFLKEEONFISANEIDNMVLIM 3586  
Db 3272 LIRYVDNRNWLKSPDGDSDQFLRWVAEVLWCKSHNFKREONFVIONEINNLAFLT 3331  
Qy 3587 PTATRRVAVTDTGTPGGGKKKKKRRDKRDKQKEVQASLMVACLKRLLPVGNLFAGRE 3646  
Db 3332 GDSKSKSKAMQ--VKSGGDQERKTKRRGDLYSIQTSLIVAALKQMLPIGLNMCTPGD 3389  
Qy 3647 QELVOHCKDRFLKMSQDVAEFAKTOLTLPDKT-DPADMSWQHLYLSKLGSKSKSNIT 3705  
Db 3390 QELISLAKRSYSYRDTDEEVEKHLRNLNLHLQESDDPA--VRQQLNLY-----KOVLK 3440  
Qy 3706 VETAENKAKIIDTVERIVAMSKVLFGMLHMDHPQOMSKNVRSVVSIOQRKRAVIAFCRQ 3765  
Db 3441 SEBPSNPEK-----TVERVQRIASAAPHLEQVEQLRSKKAVWHKLSQKRRVAVCFRM 3496  
Qy 3766 TSLHSLPRHRACNIFARTYIELWLE-EENIGQEYMIEDLTQSPEDAEKLSKSDVVEGEKP 3824  
Db 3497 APLYNLPRHSINLFLHGQRFMWETIEYSFEELVQDLAKS---PKVEEBEEMEBKQP 3553  
Qy 3825 DPLTQVTTTCRGAMTBSGALQBDPLYSYAHIIAKSC--GEBEEBGGGEBEGGEGAE 3882  
Db 3554 DPLHQIILHFSRNALTERS-KLEDPLTYTSYSSMMAKSCQSGEDEEB---EDKE----- 3603  
Qy 3883 AEDEGRASIIHEQEMEKOKLPHQARLADRGVAEMVLLHISASKGLPSEWMYKTLQLGISI 3942  
Db 3604 -----KTFEKEKEKOKTLYQOARLHERGAAEVLQMIASKGEMSPMWETILKLGIAI 3657  
Qy 3943 LRGNIDIQMGLNHLKDKDVGFFTSIAGLIMNSCSVLDLDAPERNTKAEGLGVGLEGAA 4002  
Db 3658 LNGNAGVQQKMDLYLKVXKDGAGFFQSLSGLMQSCSVLDLNAFERQNKAEGLGWTEEGT 3717  
Qy 4003 -----GEMKHDAEFTCALFRFQLTCEGHNDWQNYLRTQAGNTTVAWVITVDYLL 4056  
Db 3718 LIVREGERKVLQNDDEFTRDLFRFLQLLCEGHNSDFQFLRTQMGNTTVAWVITVDYLL 3777  
Qy 4057 RLOESINDFWYHYSSKELIDPAGKANFFKAIGVASOVFNTLTVIQCPCCTONQOALASHR 4116  
Db 3778 RLOESISDFWYYSKGDIIDESGQHNFSAKAVTQIFNSLTYEQPCIGNQOQSLASHR 3837  
Qy 4117 LWDVAGGFLFLFSHMQDKLSKHSQVLLKELNLQKDMI PMLSMLEGNVANGTIGKOM 4176  
Db 3838 LWDVAGFLHVFAWQMKLSQDSSQIELLKELLDLQDMVVMLLSLLEGNVANGTIGKOM 3897  
Qy 4177 VDTLIVESASNVELLTKYDFMFLKLKDLTSSASFOEIDANNNDGWVLPKDFKMEBQQSKYT 4236  
Db 3898 VDTLIVESSTNVEMILKFFDMFLKLKDLTSSDTPKEYPDGKGIISKKEFOKAMEGQOYT 3957  
Qy 4237 PEETEFLLACCTENHDGKLDYIGCDFRHPBAKEIGENLAVLLTNSEHPNPEPRARFL 4296  
Db 3958 QSEIDFLLSCAEADENDMFVYIDVDRFHPBAKDIGFNVAVLLTNSEHPNDSRLKCLL 4017  
Qy 4297 ETAGSVLNYPEPFLGRIEIMGSKRIERVYFEIKESNIEQWEKPOIKESKRAFFYSIVTE 4356  
Db 4018 DPRESVLNYPEPFLGRIEIMGAKKIERVYFEISESRTQWEKPOIKESKROFIDVNVNE 4077

Qy 4357 GGDKEKLEAFVNFCEDAIFEMTHASGLMAAS-----EESVGGTKNREASYM--YMGDDDD 4409  
Db 4078 GGEQEKWELFVNFCEDTIFEMQLASQISESDSADREPEEBG---DEESSVLEINGEBEE 4134  
Qy 4410 ERA--CKDPRRGLQKQVQVATAFSSLSFSNIIKAKIADMQQMPPAELAVGFFMFFYLF 4467  
Db 4135 DKSFSASAFAMACASLKRNITNLKATLKNLRKQVRNVKMTAKELVKVFFSFFMMLF 4194  
Qy 4468 YLIGYGLVVRVIFGVLL-----GLMRGPQT-----DEPPP-----BP 4501  
Db 4195 VGLFQFFFTIGVIFQILMSTVPGGLVEGAKNIRVTKILGDMPTDTQFGIHDMAEER 4254  
Qy 4502 TBEETIG---QLRHRLLA---TQSSRHLPALPPADDTQMQVSAFGLDITTKEDNGQIQV 4554  
Db 4255 AEVAEAGITTELTVHFKVGERGDTELMSDLFGLHPKEGGVKHGPEVGLGDLSLIIGK--- 4311  
Qy 4555 KPHEST--STPSSGEEAEVSPDESADHTEORPPS-LIDLGGQAKKQAQOERWEAQA 4611  
Db 4312 ---DEPPTLESTVRKKRKAQA--ETKAHEAEAGKVESEKADLEDGEKEDKAKEERAEYL 4367  
Qy 4612 AQAAMSAIEAESKKAVQGPAPALSQVDLSQYTRRAVSFLAENFYNLYKVALVLAFCIN 4671  
Db 4368 WAEVTKKKRRRGQKVEKPEAFMANFFKGLIYQTKLLHYLARNFYNLRFALFVAFAIN 4427  
Qy 4672 FVLLFYKVS--TLDGEGGSGGLGDIAGGGSGGAGSGSGSGESGDDDALEVVVHID 4729  
Db 4428 FILLFKVTEEPLEESTEDVANLW-----SLNDEEBEAMVFPVLQ 4469  
Qy 4730 EDFYMEHVIMKAAVLHISIVSLAILGYHYLKVPLAIFKREKIAKLEPDGLYIABOPE 4789  
Db 4470 ESTGYMAPTLRALAVVHTIISLVGVVYCLKVPLVVFKEKEIARKLEPDGLYITEQPS 4529  
Qy 4790 DDLKSHWKLVIJSAKSPVNYWDKFKVYKRAKYSYSETYDPSISNMLGMEKTS--PSAQ 4847  
Db 4530 EDDIKQMDRLVINTSPFHNWDFKVRKVINKYGDLYGAERIAELLDJDKNALDPSV 4589  
Qy 4848 EEBGSK--GLIHYIINIDWRYOVWKAGVTTIDNSFLYSLYWYFSYVMGNFNFFFAAHL 4905  
Db 4590 EETBAASLVSWSSIDMKYHKLGVFTDMSFLYLAWYTMVSLGHVNNFFFAAHL 4649  
Qy 4906 DVAVGFKTLRTILQSYTHNGKQLVLTVMLLTIITYTYTIAFNFFKRY-VQBEDDEVNR 4964  
Db 4650 DIAMGFKTLRTILSSVTHNGKQLVLTGULLAVVYLYTVVAFNFRKRYNKSEDDDEPDM 4709  
Qy 4965 NCHDMLTCTFVNLKYGRAGGIGDELEPPDGDSDSEVYRIIFDISPEFFTIIVILLATLO 5024  
Db 4710 KCDMMTCYLFHMYVGRAGGIGDEIEDPAGDPYEMRYIVFDITFFFVIVILLATIOG 4769  
Qy 5025 LIIDAFGEIRDOLSVKEDMESNCFICGINKOYFDKVPHGFDTHVOREHNLANYMFFLMH 5084  
Db 4770 LIIDAFGEIRDQEQVREDNETKFCIGINDYFDITPHGFTHTLQEHNLANYLFLMY 4829  
Qy 5085 LINKPTEYTGQTYVMNYTORCWDFFPVPVGCDFRKOYEDLMG 5127  
Db 4830 LINKDETEHQESYWKMYQERCMDFFPAGDCFRKOYEDQLG 4872

## RESULT 3

US-09-424-783-4  
; Sequence 4, Application US/09424783  
; Patent No. 6780608  
; GENERAL INFORMATION:  
; APPLICANT: Hakamata, Yasuhiro  
; APPLICANT: Nishimura, Seiichiro  
; APPLICANT: Barsoumian, Edward Leon  
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein  
; TITLE OF INVENTION: and DNA Molecules Coding Therefor  
; FILE REFERENCE: 0652.2000000  
; CURRENT APPLICATION NUMBER: US/09/424,783  
; PRIORITY FILING DATE: 1999-12-01  
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NUMBER OF SEQ ID NOS: 11

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LENGTH: 5037

TYPE: PR1

ORGANISM: Oryctolagus cuniculus

US-09-424-783-4

Query Match 42.3%; Score 11349; DB 2; Length 5037;

Best Local Similarity 44.9%; Pred. No. 0;

Matches 2395; Conservative 906; Mismatches 1517; Indels 516; Gaps 106;

Qy	5	EGGASEQDDVFLRTEDMVCISCTAT---GERVCLAAEGFGRNRCFLFENIAD-KNIPPD	59
Db	3	DGSEGE-DEVOFLRTDDSVLQCSATVLKEQLKCLAAEGFGRNRCFLFLEPSTNAQNPPD	61
Qy	60	LSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLCYNAILLRHLSNDMYLA	116
Db	62	LAICCFLQSLSVRALQELMANTVEAGVSSQ--GGHRTLLYGHALLRHHRMYLS	119
Qy	117	CLSTSSQ-DKLAFDVGLQHQSEACWTLHPASKQSEGEKVRVGGDDLILVAVATERY	175
Db	120	CLTTSRMTDKLAFDVLQEDATGEACWTLHPASKQSEGEKVRVGGDDLILVAVSERY	179
Qy	176	LHTTKENEVSIVNASFVHTWSVQPYGTGISEMKVGVYVFGDVLRFPHGG-DECLTIPS	234
Db	180	LHLTASGELQVDASFQMTLNMNP---ICSCCEEGYVVGHLRULFPHGHMDECLTI-S	234
Qy	235	TWTQGGQNIIVYEGGSVMSQARSILRLLEARTKWAGFINWYHPMRIRHITTYGRLGVN	294
Db	235	AADSDQRLVYEGGAVCTHARSILRLLEPLRISWGSGLRWGQPLRIRHTTYGRLALT	294
Qy	295	DONELYVSRBEATTASCAFCLRQEKDQKQVLEKDLVIGAPILKYGDSTVIVQHSET	354
Db	295	EDQGLVVVDACKAHTKATSFVRYSK-EKLDTPAKRDVEGMPPEIKYGESLFCFVQHVAS	353
Qy	355	GLWLSYKSYETKGVGVKEKQAILHEEGQMDGLDPSRQSESRARVIRKCSLIPT	414
Db	354	GLWLTAAAPDPKALRLG-VLKKKAILHQEGHMDALFLTRCQESQAARMIHSTAGLYN	412
Qy	415	KFINGLETQENRRHSMFFA--SVNLGEMVWCLDELINLYFAQPDMEHEKQNKFRALR	472
Db	413	QFIKGLDSFGSKPRGSGPPAGPALPIEAVILSLQDLICFYFPPEELQHEKQKLSLR	472
Qy	473	NRQDLFQEGILNLILEAIDKINVITSQGLAGFLAGDESQSMESIGYLYQLAAIIR	532
Db	473	NRQSLFQEGMLSLVNLICIDRLNVVYTAHFAEY-AGEEAAESWKEIVNLLYELLASLR	531
Qy	533	GNHTNCAQFANSRLNWLFSRLGS-OASGEGTGMLDVHLCHVLIDSPEALNMRRDEHIKI	591
Db	532	GNRANCALF--STNLDWVSVKLDRLAS--SGILEVLYCVLIESPEVNLIIQENHKS	586
Qy	592	ISLLEKHGRDPKVLVDLCSLCVGVAVRSNNICDVLPGKMLLQTLALVDHVSSVRP	651
Db	587	ISLIDKGRNKHVLVDLCSLCVGVAVRSNQDLITENLLFQRELLQTNLINVYTSIRP	646
Qy	652	NIFVGRVGSVYRKWYFVETMDHIEK-TTHMPLHRIGWANTTGYVPYGGGKMGNG	710
Db	647	NIFVGRAGSTQYKWKYFVEMVDEVVVPFLTAQTHLRVGMALTEGYSPPGGGEGGNG	706
Qy	711	VDDLYSGFDGAYLWMSGRKTPVNRTHAEPYIRKGDVIGCALDLTVPIINFMNGVRV	770
Db	707	VDDLYSGFDGLHLMTGHVARPV--TSPGQHLAPEDVWSCCLDLSVPSIFRINGCPV	764
Qy	771	TGSEFTNENLGFVPIVSCSKLSRFLGEGHRLRYAABEGYSPVLESILLPOOILSL	830
Db	765	QGVFAFNLDGLFFPVVSFAGVKVYFLLGGHGEFKFLPPGYPACHEAVLPRRLRL	824
Qy	831	PCFYGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTVVEQIRKLAENIHEMMAM	888
Db	825	PIKEYREGPRGPHLVGRSCLSHTDFFVPCPVDTVQIVLPHLERIREKLAENIHELWAL	884

Qy	889	NKIEAGWYGDQREDLHKIHPCLVPPFRLPPAERKYDIQAVQTLKTILALGYISL--D	946
Db	885	TRIEQGWYGPVRDDNKRHLHPCVLNPHSLPERNYNLQMSGETLKTLLALGCHVMADE	944
Qy	947	KPPARIRNVLNPNPPMQSGNGYKAPLDLSAVTLTPQMDLVDLAENTHNLHAREIQ	1006
Db	945	KAEDNLKTKLP-KTYMMSNGYKAPLDLSHVRILTQAQTLVDRLAENGHNVDWARDVAQ	1003
Qy	1007	GWYGLNEDSDMHSRPHLVYKPVDDAIKKAANDTASSETVRTLLVYGYMLDPPPTGEQEA	1066
Db	1004	GWYSIVQDIPARRNPLVYRLDDEATKSNRDSLCOAVRTLGYGYNIEPPDQES--	1061
Qy	1067	LLLEASKQKQAD-FRTYRAEKNYAVSSGKWFYFEILTAGPMRVYGAHADMAPGMMLQD	1125
Db	1062	--QVENQSRWDVRIFRAEKSIVTQSGRWYFEFAVTTGEMRVGMARPELRPDVLCAD	1118
Qy	1126	ENSWAFDGYNEEKVYSGNTESFGKQWAGDVGVFLDLIDKTTISFSLNGELLMALGGET	1185
Db	1119	ELAYVFNHGRQWHLG-SEPFGRPMQSGDVGVGCMIDLTTENTIIFTLNGEVLMSDSGET	1177
Qy	1186	TFADVQ-GDNFVPACTLGVGQKARLTVQDVTNLTLYFTTCLOGBGYEPPFCVNMKRDVTHW	1244
Db	1178	AFREIEIGDGLPVCSLGPGQVGHNLGQDVSSLRFFAICLQGBGFPAFALNMORPVTTW	1237
Qy	1245	YTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLIKISHNTFTETMEK-ANWEFLRLSPVI	1303
Db	1238	FSKSLPQFEPVPE-HPHYEVARMDGTVDTPCLRLAHTWGSQNSLVEMFLRLSLPVQ	1296
Qy	1304	CHNEFIDEAKRWWIEIKORQILMKEAVEAOMPAAHDIQIMRSGFTWIDIKGLHYEDNQ	1363
Db	1297	FHQHFRCTA-----GAT-----	1308
Qy	1364	ELPSSKWKRLPSRPRKSGMTRGTIYNNYLQPGVQVNGMHRSTSEAMAKYDLGAQGL	1423
Db	1309	-----PLAPP-----GLQP-----PADE-----ARAA	1326
Qy	1424	TPDDKDKRGRSPKFRSRKRGESSDRAKSKTDPDPFSDTEVSPERGARRPNQIKVS	1483
Db	1327	EPDPDYENLRSSAGCGEAGEGEGTAKETPGTGPQ--GVEAQP--VRAENEKQATT	1381
Qy	1484	QANQRYNGMARPSRTNLYGSQVGLNATPQDRKQMTTSTAQSATETV-GNEIFDAEC	1542
Db	1382	EKNKK-----RGFLFAKKAAMWTPP-----ATPALRPLPHDVPADNRDDEI	1426
Qy	1543	LKLINEFYGVRIYPGODPTHVYIGWTTQVHLHSKDFNOSKVTSSVIIITDDYDVVEN	1602
Db	1427	ILNTTYYVVRVYAGQEPSCVWGVWTPDYHQHDMFDSLKVRAVVTMGDEQGNVHSS	1486
Qy	1603	VNROSCYVRADELYNEVMAEATAKASQGMFICGSVDSTSGVSFTCEGKDTSFKFKME	1662
Db	1487	LKSCNRYWGGDF--VSPQOQGRISHTDLVIGCLVDLATGLMTFTANGKESNTFFQVE	1543
Qy	1663	PETKLPFAIVFEATSKELQIELGRSATSPLSAVLPTSDKHVIFOPPPRLKQVCLKPH	1722
Db	1544	PNTKLPFAVFLPTHQVNIQFELGKQKNIMPLSAAMFLSERKNPAPCPPLRLEVQMLPV	1603
Qy	1723	QWARPVQSLQVHALKLSLDIRGWSMLCEDAVSMLALHIPEDRCIDILEPIEMDKLLSPH	1782
Db	1604	SWSRMPNHFLOVETFRAGERLGWAVQCODPLTMMALHIPENRCMDLLELSERLDQRFH	1663
Qy	1783	SHTLTLAALCYQSNYRAAALCTHVQKQLLYAIQSOYMSGRLRQGFYDLILLALHLESH	1842
Db	1664	SHTLRLRVACALGNRRVAHALCSHVQALHDAHLPLPLRAGYDILLISHLESA	1723
Qy	1843	ATTMEACKNEFVPLGPPELKALYBEPP-----MHSRLSL-OTESVRPQMKMTD----	1890
Db	1724	CRSRRSLSEVIVPLTPETRAITLTPPGKGNARRHGLPGVGTTSRLRPHHFSPPCFV	1783
Qy	1891	---IAESITEISNLYSPFFLEVAREFVMOALAEAVETNOVHNRDPVCGSNENFLPLIK	1947
Db	1784	AALPAAGVAEAPARLSIPAIPLEALRDKALRMGLGEAVRGGQGHARDPVGSGVEFQVPVLK	1843



Db 3899 FONYLRQTQNTTINIICITVDYLLRLQESISDFWYYSKDVIEQCKRNFSAKMSVA 3958  
Qy 4091 SOVENTLTVTOGCTQNOALASRLNDVAGGFLFLFSHMODKLSKHSQVDDLKELLN 4150  
Db 3959 KOVFNLSLTXTOGCTQNOALASRLNDVAVGFLHVFHMMWMLKQAQSSQLELLKELLD 4018  
Qy 4151 LQKDMIPMMLSLMGLGNVNGTIGKQWDTLVESASNVLLILKYFDMFLKLDLTSSASFQ 4210  
Db 4019 LQKDMVWMLLSLGLGNVNGIARQWDMVLVSSSNVEMILKFFDMFLKLDIVGSEAFQ 4078  
Qy 4211 EIDANDGWLPKOPKKEQKQSVTPBEIIFPLACCTNHDGKLDYIGFCDRPHEPAKE 4270  
Db 4079 DYTDPGRGLISKDKQAMDSOKQTGPEIQFLLSCSEADENEMINPEEFANRFOEPARD 4138  
Qy 4271 IGFNLAVLLTNLSHMPNEPLRLALETAGSVLVNFFPLGRIETMGSKRIERYVPIK 4330  
Db 4139 IGFNVAVLLTNLSHVPDPRLNFLEAESTILEYFRPYLGRIEIMGASRIERYFIS 4198  
Qy 4331 ESNTIEQWEKPOIKESKRAFFYSIVTEGGDKKELAFVNFCEDAIPETHASGLMAASBS 4390  
Db 4199 ETNRAQWEMPQVKESKQFIDVNVNGBEAKWELFVSFCEDTIFEMQIAAQISEPEGE 4258  
Qy 4391 VGGTKNRBASVYMGDDDDERAGKDPFRRGIQSVKDG-----V 4428  
Db 4259 -----BA-----DEDEGNGE-----AAAGABEGAAGAAAGTVAAGATARLAAA 4300  
Qy 4429 ATAFSSLSPSNIIKAKIADMQWPPPAELAVGFFKMFYLYLYG-----GVLVVRYIYGV 4484  
Db 4301 ARALRGLSYRSLRRVRLRLRTAREATAALWAVVARAGAGAGAAAGALLRLWGS 4360  
Qy 4485 LL--GLMGPO---TD--ERPEPTEBEKIGOLRHLRLATQSSRHLPALP--PADDTGO 4534  
Db 4361 LFGGLLEGAQKVTVELLAGHDPDTSDEVHGE-----QPAGGGDADGAGE 4407  
Qy 4535 MQVSFAFGLDITKEDNGQIQVKPHES----- 4559  
Db 4408 GE---GEGDAAGDEGEVAGHGAEGVAVADGGPRPBGAGGLGDMGDTTPAE 4463  
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Db 4464 PTPGSGPILKRLKLGVDGEEELVPE---PEPEPEPEKADENGE---KEEVPB----- 4513  
Qy 4611 AAQAAMSAIEAESKKAQVGPAPSALSQV-----DLSQYTRRAVSFLARFNYLK 4660  
Db 4514 -----APPEPPKA---PPSPPAKKEAGAGMEFWELEVQRKFLNLSRNFYTLR 4563  
Qy 4661 VVALVLAFCINFLVLYKYSTLDGEG---EGSGLGDIAGGSGSGAGSGGSGGES 4716  
Db 4564 FLALFLAFLAIFILLFYKVS--DSPGEDDMGSAAGD--LAGAGSGSGSGWAGGABAE 4620  
Qy 4717 GEDDALLEVVIHDEDFMEHVIRKMAVLHSIVSLAIIIGYHLKVPILAIFKREKEIARK 4776  
Db 4621 GDEENVMVYFLEESTGYMEPALWCLSLHLTLVAFLCIIGVNCVPLVIFKREKELARK 4680  
Qy 4777 LEFDGLYIAOEPPDDDLKSHMDKLVISAKSPVNVWDFKVKVAKYSETVDFDSINM 4836  
Db 4681 LEFDGLYITEQGGDDVQGWDRVLVNTSPSPSNVWDFKVRKRLVDKHGDIPIGRIRIAEL 4740  
Qy 4837 LGM-----EKSFSQAQEEGSKGLIHYIINIDWRYQVMKAGVTITDNSFLYSLWYFSPV 4891  
Db 4741 LGMDLASLEITAHNERKPPPPGLLTWLSIDVKYQIMKFGVIFTDNSFLYLGWYVWMSL 4800  
Qy 4892 MGNFNFPFAALLDVAVGFKTLRTLOSVTNGKQLVLTWMLLTIIIVYIVTVIAFNFR 4951  
Db 4801 LGHNNFPFAALLDIAMGVKTLRTLOSVTNGKQLVMTVGLLAVVYLYTVVAFNFR 4860  
Qy 4952 KFWQEEED--DEVNRNCHMDLTCFVNLYKGVAPAGGIGDELEPPDGDSDSEVRIIFDISF 5010  
Db 4861 KFYNSKSEDEPDKCDDMMTCYLFHMYGVVGRAGGIGDEIDPDAGDEYELRVVVDITF 4920  
Qy 5011 PFFITVILLAILOGLIIDAFAGBLRQLESVKEDMESNCFICINIKDYFKVPHGPDTHVQ 5070  
Db 4921 FFFVIVILLAILOGLIIDAFAGBLRQOQOEKEDMETKCFICIGISDYDPTTPHGETHTL 4980

Qy 5071 REHNLANYMFLMLINKPDEYTGQTYVVMNMYTORCWDFPVPVGDGCRKQYED 5124  
Db 4981 EEHNLANYMFLMLINKDEHTGQESYVWKYQERCWDFPVPVGDGCRKQYED 5034  
RESULT 4  
US-09-538-092-979  
; Sequence 979, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
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; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuratPatSeqformatter Version 0.9  
; SEQ ID NO 979  
; LENGTH: 5032  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number P21817  
US-09-538-092-979

Query Match 42.3%; Score 11325.5; DB 2; Length 5032;  
Best Local Similarity 44.9%; Pred. No. 0;  
Matches 2394; Conservative 895; Mismatches 1531; Indels 513; Gaps 102;

Qy 1 MAEAGGAS EDDYSLRTEDMCLCTAT---GERVCLAAEGFGNRHCFLENIAD-KN 55  
Db 1 MGDAG-----EDVQFLRTDDVVQLCSATVLEKQLKCLAAEGFGNLCLEPSTNAQ 56  
Qy 56 IPPDLSQCVFIEQALSVRALQELV---TAAGSTGKTGSGHRTLLYGNAILRLHNSD 112  
Db 57 VPPDLAICCFVLEQSLSVRALQELANTVEAGVSSQ--GGHRTLLYGHAILLRHAHSR 114  
Qy 113 MYLACLSTSSQ-DKLAPDVGLQHSQGEACWTLHPASKQORSEGEKVRVGGDILLVSA 171  
Db 115 MYLSCLTTSRSMTDKLPDVLQEDATGEACWMTMHPASKQORSEGEKVRVGGDILLVSVS 174  
Qy 172 TERYLHTTKENEVSIVNASRHTVTHWSVOPYGTGTSRMKYGVGVGGDVLRFPHGG-DECL 230  
Db 175 SERVLHLSTASGELOVDASFMQTLWNMPI---CSRCE-EGFVTGGHVLRFLHGHMDECL 230  
Qy 231 TIPSTWTKDGGQNTVVYEGGVSMSQARSRLRLELARTKWAGGFINWHPMRIRHTTQRY 290  
Db 231 TI-SPADSDQRRLLVYEGGAVCTHARSRLRLEPLRISWSGSHLRWGQPLRVHRVTTQY 289  
Qy 291 LGVNDQNELYLVSRREATTASACFLROEKDDQVLEDKDLEVIGAPIIKYGDSTVIVQ 350  
Db 290 LALTDEQGLVVVDASKAHTKATSCFRISK-EKLDVAPKRDVGGMGPPPEIKYGESLCFVQ 348  
Qy 351 HSETGLMLSYKSYETKKKGKVKREKQAILHEEGKMDGLDFSRSQEESRTARVIRKS 410  
Db 349 HVASGLWUTYAAPPKALRLG-VLKKQAWLHQEGHMDALSLTRCQEQESQARMIHSTN 407  
Qy 411 SLFTKFLNGLETLOENRHS--MFFASVNLGEMVCMLEDLINYFAQPDDEMEHEKQNF 468  
Db 408 GLYNQFIKSLDSFSKPRGSGPPAGTALPIEGVILSLQDLIIYFEPPSEDLQHEEKSQL 467  
Qy 469 RALNRNQLFOEBEGLNLILRAIDKINVITSGQFLAGFLAGEGSGQSHMISGYIQLLA 528  
Db 468 RSLNRNQLFOEBEGMLSVLNCIDRLNVYTTAAHFAEF-AGEEAESKEIVNLLYELLA 526



Db 2504 FLDRVYGIENQDFLLHVLVGVFLPDMRAAASLDATATFTTTEWALAVNRYLCLAVLPLITK 2563  
Qy 2658 HAYFYNEAENVASLADLHTVYRLSKNMLTKGQREAVSPFLVALTSAMOPSMMLKLLR 2717  
Db 2564 CAPLFAGTEHRAIMVDSMLTYRLSRGRSLTKAQRDVIEDCLMSLCRYIRPSMLQHLR 2623  
Qy 2718 KLTVDVSKLSEYTTVALRLLTLHYERCAYKYGSTGAGQAFASDEKRLTMMLFNSIF 2777  
Db 2624 RLVDVDPILNEPAKMLKLLTNHYERCWKY--CLPTGWANFGVTSSEELHLTKLFWGIF 2682  
Qy 2778 DSLKMDYEPFLFGKALCLIAIGCALPPDYLSKNYDDEFYVGEQAAGDLD--NPQYDPQ 2836  
Db 2683 DSLAHKKYDPELYRAMPCCLCAIAGALPPDY-----VDASYSKAEKATVDAENFDP 2737  
Qy 2837 PLNTSSVALNNDLNTIVOKFSBHYHDWASRKIENGWYVGEWSDSKTHPRLKPYNNLN 2896  
Db 2738 PVETLNVIIPEKLDSEFNKFBYTHEKWAFDKIQNNWYGENI DELKTHPMLRYKTF 2797  
Qy 2897 DYKERYKEPVRESIKALLAIGWSEVHEGEVDIPSNRRSMRQSKSGRPPPIVTDATP 2956  
Db 2798 EKDKIIRWPIKESLKAMIAEWTE-----KAREGEEKTEKKTKAKISQSAQT 2847  
Qy 2957 PD-----YNHPVDVMTNLILSRMKNMAERLADNAHDIAWAKKKEBLVTNGGIIHPOLVPY 3012  
Db 2848 YDPREGYNPPDLSAVTLRSLEQMAEQLAENYHNTWGRKKQBLEAKGGGTHPLLVY 2907  
Qy 3013 DLLTQKKEKKRERQOEFKYLQYGYKLHRSKAPQSDTEQTTTGVAIELRFAYSLLEK 3072  
Db 2908 DTLTAKEKARDREKAQELLKFLQMGYAVTRGLKOMEIDSS-----SIEKRFAGFLQQ 2961  
Qy 3073 LTQYDTRATINMKLAK--PSTTFSRRSPKTRDRIKFFSKAVLPLMEKYFSTRNYFIA 3130  
Db 2962 LIRWMD---ISQEFTHALEAVSSGRVEKS PHEQEIKFPAKILLPLINQYFTHCLYFLS 3018  
Qy 3131 V-ATATNNVGAASLKEKEMVAALFKLASLLRSRAAFQPDVRIIVTRCLQVLVKGIDAKS 3189  
Db 3019 TPAKVLGSGGSHASNEKEMITSLFKLAALVHRVSLFGTDAPAVVNCILHILARSILDART 3078  
Qy 3190 LVKNCPEFIRTSMLTFNNVADVGHITMNLQDGYVAHLRGTHLKTSTSLGVINGVLLPI 3249  
Db 3079 VMKSGPEIVKAGLSRFFESASEDIEKMNENLGLKVQSQARTQVKGQNLTYTTVALLPV 3138  
Qy 3250 LTAKEFDHLANCYBGADLLDETQVASYKMLGSLYALGDASLTHDRKYLKTEIERHKPAL 3309  
Db 3139 LTTLFQHIAHQFGDDVLDVQVSCYRCLCSYLSLGTKN-----TYVEKLRPAL 3189  
Qy 3310 GSCLGAFSSTFPVAFLEPHLNKHNFSLNRIADHS---LEAQDMQKMEQCMPTLETIL 3366  
Db 3190 GECLARLAAAAMPVAFLEPQLNBYNACSVYTTKSPRERAILGLPNVSEEMCPDIPVLERLM 3249  
Qy 3367 GEVDQFVESDKTYNEAPHIIDVVLPLLCYSLFPFWAAGPD---NVTPTGG-NHVTWVTAE 3422  
Db 3250 ADIGGLAESGARYTEMPHVIEITLPLMCSYLPFRWMERGPEAPSPALPAGAPPCTAVTSD 3309  
Qy 3423 HNNOLLKNVLKLIKKNIGNENAPWTRIATYTOIINSSEELLRDSFPLAERYVKRTD 3482  
Db 3310 HLNSLLGNLRLIIVNMLGIDEASWMLKRLAVFAQPIVSRARPELLQSHFPTIGRLKRAAG 3369  
Qy 3483 NMFHKEESLRGTKSTDDTSQVESQIQBDWOLLVRDIYSFYPLLIKYVDLQORNHLRNN 3542  
Db 3370 KVVSEEEQLALEKA---EAQGEGLLVRFDEFVLCRDLVALYPLLIYRYVDNNRAQWLTEP 3426  
Qy 3543 VPEAEELYNHVAIFINWKSQVFLKEBQNFISANEIDNMVLIIMPTATRTVAVTDGTTPQ 3602  
Db 3427 NPSAEELFRMVGEIFTYKSHNFKEEQNFVQNEINNMSFL--TADNK-----SKNAK 3479  
Qy 3603 GGGKXKXKRDKRDKXKQVQSLWVACLKLLPLVGLNLFAGREQELVCHQDRFLKXKS 3662  
Db 3480 SGGSQDERTKKRRDRYVSQTSLVATLTKMLPIGNNCAPTDQDLITLAKTRALKOT 3539  
Qy 3663 EODVAEFAKTQTLTPKIDPADEMMSQHYLYSKGSKSNITVETAENKAKIIDDTVER 3722  
Db 3540 DEEVREFLHNNLHQKRGVSGSLRWOMALYRGVPGRE-----EDADDEPEKI----VPR 3589

Qy 3723 IVAMSKYFLGLHMTIDHPQOMSKNRYSVSVSIQRKRAVIACFRQTSLSLSLPHRAACNIFAR 3782  
Db 3590 QVEVSALVLYLDQTEHPYKSKKAVWHKLLSKQRRRAVAVCFRMTPLYNLFTHRACNMFLE 3649  
Qy 3783 TYTELW--LEENIQOEVMIEDLTOSFEDAELKKSDVVVEEGEKDPDLTQLVTTFCRGAWTE 3841  
Db 3650 SYKAAWILTSDHSPEDRMIDDLKAGQEE--EEEEVEE--KKPDLHLQLVLFHFSRTALTE 3706  
Qy 3842 RSGALQBDPLMYSAHIIAKSCGEBEGEGEGEAEAEDEGRASIEHQEMEKOKL 3901  
Db 3707 KS--KLDELYLYMAVADIWAKSC-----HLEEGGEGEAEEVEVSPPEEKQWQKRL 3756  
Qy 3902 LFHQARLADRGVAEMVLLHISASGLPSEMVMKTLQGISILRGNDIDIOGMNLHLKDK 3961  
Db 3757 LYQCARLHTRGAABWMLQMSACKGETCAMVSSTLKLGISILNGNAEVOQKMLDYLKDK 3816  
Qy 3962 KDVGFFTSIAGLNNSCSVLDLDAFERNTKAEGLG-VGLEGAA-----GEKNHDAEFTCA 4015  
Db 3817 KEVGFQSIQALMQTCSVLDLNAFERQNKAEGLGMVNEDEGTVINRQNGEKYMAODEFTQD 3876  
Qy 4016 LFRFIQLTCEGHNDWONLRTQAGNTTNNVVTCTVDYLLRLOESIMDFYMYHSSKELI 4075  
Db 3877 LFRFLQLLCEGHNDWFQNYLRTQGTNTTINIICTVDYLLRLOESISDFYMYSGKDI 3936  
Qy 4076 DPAGKANFFKAIGVASQVFNLTLEVIQGPCTQNOQAALSAHSLWDVAVGFLFLFSHQDKL 4135  
Db 3937 EEQKRNFSKAMSAKQVFNLSLTVIQQPCTGNQOQSLAHSRLWDVAVGFLHVFHMMML 3996  
Qy 4136 SKHSQVDLLKELNLKQDMIPMLSLMEGVNVGTICKQNVDTLIVESAASVLLIKYFD 4195  
Db 3997 AQDSQIELLKDLQDMVYMLLSLLEGVNVGMARQVMVLMVLESSNVEMILKFFD 4056  
Qy 4196 MFLKDLKLTSSAQEIDANNQWVLPKDPKEKMEQOKSYTPPEIEFLACETNHDKL 4255  
Db 4057 MFLKDLKLTGSEARQDYVTDPRGLISKDFOKANDSQFQSGPEIQFLLSCSEADENMI 4116  
Qy 4256 DYICDRFHPFAKEIGFNLAULLNLSEHNPRLARFLETAGSVLNYFEPFGRIEI 4315  
Db 4117 NCEEFANRFQEPARDIGFNVAULLNLSEHVPDPRLHNFLELAESILEYFRPYLGRIEI 4176  
Qy 4316 MGGKRIERTVFEIKESNIEQWEPQIKESKRAFFYSIVTEGGDKKELEAFNFCEDAIF 4375  
Db 4177 MGASRRIERIYFSETNRAQWEMPQVKESKROQIFDVVNEGGEAKRMLFVSCEDTIF 4236  
Qy 4376 EMTHASGLMAASEESVCGTKNREASYMYMGDDDERACKDPFRRGLQSVQDGA----- 4429  
Db 4237 EMQIAAQISEPEGEP-----ETDEDEGAG--AAEAGAEAEAGAELEGTA 4280  
Qy 4430 -----TAFSSLSPSNIIKAKIADMQMPAPBLAVGFFHFFYLYLYGVG 4473  
Db 4281 ATAAAGATARVVAAAGRALRGLSVLSRRLRRVRLRLTAREATAVAALLMAAVTRAGAA 4340  
Qy 4474 VLVVVRYIFGVLLGLMRGQFQTDDEPP-----PEPTEEKIGQLRHLLATQSSR 4521  
Db 4341 GAGAAAGALGLLWSLFGGLVEGAKKVTVTTELLAGMPDPTSDEVHGE----- 4388  
Qy 4522 HLPALPPADDTGQWQVSFAFLDIYKEDNGQIQVXPHE----- 4559  
Db 4389 -QPAGPGGDADG--EGASEGADGAABGDBEEAVHEAGPGGADGAVAVTGGPPRPEGA 4445  
Qy 4560 -----PSTSTSSGEEAEVSP-----DESADHTEQRPPLSLDLGGEQAKKQAOERMEAQ 4610  
Db 4446 GGLGMDGDTTFAEPPTPGSPILKRLKLVGDVGVHEELPPE----PEPEPEPELEPEKADAE 4501  
Qy 4611 AAQQAAMSAI EAESKAVQGPAPSALSQV-----DLSQYTRRAVSFLARFYNLKVYA 4663  
Db 4502 NGKEEVEPTEPPPKKQAPSPPPKKEAGGEFWELEVRQVKPLNLSRNFYTLRFLA 4561  
Qy 4664 LVLAFCINPVLLFYKVTLDGEGG-----EGSLGDI IAGGSGSGAGSGSGSGESQBD 4719  
Db 4562 LFLAPAINFILLFYKVS--DSPPGDDMEGSAAGDV---SGAGSGSGSGWGLGAGEABEG 4616





QY 1299 SLPVICHNEFIDEAEKARRWEIKDROQILKMEAVEAQMPAHIDQIMRSGFTMNDIKGLH 1358  
 Db 1292 SMPVECHSSF----- 1301  
 QY 1359 YEDNOBELPSSKMKKLPSPRPKRGWTRGVTIQNNNNOPGOVNGMHRSTSEAEWAKYDL 1418  
 Db 1302 ----- 1301  
 QY 1419 GAQGLTPDDKDKRGSRPFKFRS KRGSDDRAKSRKSTDPDFSDTEVS PERGARPNP 1478  
 Db 1302 ----- SHSPCLDSEA----- 1311  
 QY 1479 QIKVSOANQYNGMGNARPSRTNLYGSQVGLNMATPDQRKQMTTSLAQSAETETVGNBIF 1538  
 Db 1312 ----- FQKRKQM-QEILSHTTT----- 1327  
 QY 1539 DAECUKLINEYPYGVRIYPGQDPHYVIGWVTTQVHLHSKDPNQSKVTKSSVITDDYDR 1598  
 Db 1328 --QC-----YYAIRIFGQDPPSCVWVGVWTPDYHLYSEKFDLNKNCVTVTVLGDERGR 1378  
 QY 1599 VVENVNROSCYMRADLEYNEVMAEATAKASQGMFICGSVDTSVSGSFCEGKDTSEK 1658  
 Db 1379 VHESVKRNCYMWGGDI---VASSQRNRSNVLDLEIGCLVDLWGMGUSFANGKELGTC 1435  
 QY 1659 FKMEPETKLPFAIFVEATSKEILQIELGRSATSPLSAVLPTSDKHVIPPFPPLKVCQ 1718  
 Db 1436 YQVENTKVFAVFOPTSTSLFQFELGKLNAMPLSAAIIRSEBENVPVQCPRLDVQT 1495  
 QY 1719 LKPHQWARVPNQSLOVHAKLSDIRGWSMLCEDAVSMLALHIPEDRCIDILEPIEMDKL 1778  
 Db 1496 IQPVLWSRMPNSFLKVETERVSERHGVVQCLEPLQNMALHIPENRCVNDILECEQEDL 1555  
 QY 1779 LSPFHTLTLYAALCYQSNYRAAHALCTHVDQKOLLYAIQSOYSGPLRQCFYDLILALH 1838  
 Db 1556 MRFYHTLRLYSAVCALGNSRVAYALCSHVDSLQSLFYAIDNKYLPGLLRSGFYDLILSIH 1615  
 QY 1839 LESHATTMEACKNEFVILPLGPBLK--ALYEEPDGMGHSRLSRLQTES-VRPQMKMTDIABSI 1895  
 Db 1616 LASAKERKLMKNEVILITITSITRNICLPDBSKHGLPGVGLRCLCPGRFRFSPCFVV 1675  
 QY 1896 T-EISNLSYPPELVAREFVMOALAAEVETQVQVHNRDPVGGSNENLFLPLIKLVDRLLL 1954  
 Db 1676 TGEDHQKSPETPLESLRTKALSMLETAQVCSGAHIRDPVGSVBFQVFPVLKJGTLLV 1735  
 QY 1955 VGMWDEDEKLLIWNTPETWD-----PSFDKSGKDEHRKGL 1991  
 Db 1736 MGVPDDDDVRQILLIDPSVFGESAGTEBGAEBKBEVTOVEKAVEAGEKAGKAPVKGL 1795  
 QY 1992 LHMKAEGAKLQMCYLOHLNDIQLRHRVEAIIAFADHFVGDLOTDLRRYTEIKQS-DL 2050  
 Db 1796 LOTRIPESVKLQMCCELLSVLDCLOHRVEAIVAGDIYVSKLOANQKFRYNELMQALNM 1855  
 QY 2051 PSAAAKTTRPCPPREOMNAILSPKHLSEEDKENCPCGEBELIARMNEFHTLMAHVS 2110  
 Db 1856 SAALTARKTKFSPPEQINMLNF----QLGENCEPCPEIRBELYDFHEDLLHCGV 1910  
 QY 2111 HALQPDAAENQPEAKPQAFKLYNIINTVKELESEAKAIEPPKPTPEEK-----F 2163  
 Db 1911 -----PLUEEBEEDTSSWTGKCALVYKI-----KGPPKPEKEQTEEBEERCPTTL 1957  
 QY 2164 RKVLQTIVNVAESQIETPKLVREWFSLVRQYDAVGELIRALEKTYVINAKTKLDVAE 2223  
 Db 1958 KSLISQTMICWAOEQIQDSELVRMFLNRLRQYDSIGELLOALRKYTISHTVSVDIIN 2017  
 QY 2224 MWVGLSQRALLPVQMSQEEELMRKWLKVNHTFFQHPDLIRLVRVHENVMVAMNT 2283  
 Db 2018 LLAALQIRISLLSVRMGKEELLMINGLDIMNNKVYQHPNLMRVLGMHETVMEVMNV 2077  
 QY 2284 LGRRAQAQSDAQPSSQPVADSEKDDTSHVMVACCRFLCYFCRTGRQNOKAMFDFPL 2343  
 Db 2078 LG-----TEKSQIAPPKMVASCCRFLCYFCRISRQNOKAMFHL Syl 2119  
 QY 2344 LENSNIILSRPSLRGSTPLDVAISSYSSMENTELALALREHYLEKIAVYLSRCLQNSSELV 2403

Db 2120 LENS SVGLASPSMRGSTPLDVAASSVMDNDELALSLEEDPDKVVTYLAGCGLQSCPMLL 2179  
 QY 2404 EKGVPDLGMDPVEGERYLDLFRFCVWVNGESVENANLIRLLIRRRPECGLPALRGE-GE 2462  
 Db 2180 AKGVPDVGWNPITEGERYLSFLRFAVFNSESVEENASVVVKLLIRRRPECFPALRGE 2239  
 QY 2463 GLKAIIVDANKMSR-----IADRRKLRMEQEGGVNFSHPLPSEDEDEDYDITGAALNF 2518  
 Db 2240 GLLAAMQGAIKISENPALDLP SQYKEVSTEDD-----EEEEIVHMGNAIMSF 2289  
 QY 2519 YCTVLILGRCAPDAGVIALGKNEESLARAILRSLVPLEDLOGVLSRFTLNNPAAGEER 2578  
 Db 2290 YSALIDLGRCAPEMHIQTKGGAIRISIRSLVPTEDLVGIIISIPKL--PSLNKDG 2347  
 QY 2579 PKS--DMPSGLIPGHKQSGVGLFLEVRVGIETQELFYKLEBEAFPLDRAAATMLDRNDGCE 2636  
 Db 2348 SVSPEDMAGNFCPDHKA PMVLFDRVYIGIKQOTELLHLLVGVFLPDLRASAISLDTVSLST 2407  
 QY 2637 SDMAISNRNYIGNSILPILIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTQGOBEAV 2696  
 Db 2408 TEAALANRYICS AVLPILTFECAPLFGGTEHCTSLIDSTLQTIYRLSKGRSLTKAQRDTI 2467  
 QY 2697 SDFVALTSAMQPSMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYGSTGACQG 2756  
 Db 2468 BECLLAICNHLRPSMLQOLRLRVDFVDPQLNEYCKMPLKLTNHYEQCKY-CLIPSGWG 2526  
 QY 2757 AFGASSBEKELTMMFLSNFDSLSKMDYBEPFEGKALPCLIAIGCALPPDYSLSKNYDD 2816  
 Db 2527 SYGLAVSEELHTEKLPWGIIDLSHKYKDDPFLRMAIPCLSAJAGALPPDY-----JDS 2581  
 QY 2817 EBYG--KEQAGDLDNDPQDPQIPINTSSVALNNDLNTIVQKFSHYHDAMASRIENGWV 2874  
 Db 2582 RITATLEKQISVDADG-NFDPKPIINTWNFSLPEKLEYIVTKYAEHSHDKMACDSQSKW 2640  
 QY 2875 YGEGMSDSQKTHPRLPKPNMNDYKERYKEPVRESKALLAIGNSVEHSE-----VDIP 2929  
 Db 2641 YGISLDENVKTHPLIRFPKLTLEKEKITYRPAESLTKMLAVGTVERTKEGALVQOR 2700  
 QY 2930 SNFSSMRQSKSGRPPEIVTDSATPPDYNPHVDMTNLTLREMONMARLADNAHDI 2989  
 Db 2701 ENELKRSVSQANQN-----SYSPAPDLJNSNVLSRELQMGVEVAENYINI 2747  
 QY 2990 WAKKKKEBELVTNGGIHPQLVPYDLDTKEKKDRERSQEBFLKYQGYKLRHPSKAPQ 3049  
 Db 2748 WAKKKLELESKGGSHPLVPYDLTAKEFKDREKAQDLFKFLQVNGIIVSRGMKOME 2807  
 QY 3050 SDTSQTTTGVVAELRFPAYSLEKLIQYIDRATINMKLKPSTTFSRRSSFT--STRD-- 3105  
 Db 2808 LDAS-----SMEKRFYGFYKILKYVDSQAQETIAHLEAIV-----SSGKTESPRDQE 2856  
 QY 3106 IKFESKAVLPMEKYFSTHRNYFI-AVATATNNVGAASLKEKEMVAALFKCLASLRSRL 3164  
 Db 2857 IKFPAKVLPLVDQYFTSHCHYFLSSPUPKJUSSGSHKEMVAGVFCUKLAALVRURI 2916  
 QY 3165 AAFGPDVRITVRCLOVLVKIGDAKSLVKNCPEFIRTSMLTFNNVADDVGHITMNLQDGK 3224  
 Db 2917 SLFSDSTWVSCHLILAQTLDTRTVMKSGSELVKAGLRAFFENAAEDELKTSNKLKG 2976  
 QY 3225 YAHLRGTHLK-TSLSLGYINGVLLPILPAKFDHLANCCEYAGADLLDEITQVASYKMGSLY 3283  
 Db 2977 FTHSR-TQIKGVQSNVINTVALLPILTSIFEHVTQHOGFMDLLIGDQVQISCHYILCSLY 3035  
 QY 3284 ALGTDASLTHDRKYLKTEIERHKBALGCLGAFSSTPFALEPHLNKNHOFSLNRIAD 3343  
 Db 3036 SLGTGKNI-----YVERQORFALGECCLASLAAAIPVAFLEPTLNRNPLSVNTKTP 3086  
 QY 3344 HS---LEAQDQIMQNEQCMPTLETILGVEDQFVESDKTYNEAPHIIDVVLPLLCSYLPFW 3400  
 Db 3087 RERSILGMDPTVEDKCPDIPQLEGMLKINDLASEGARYTEMPHVIEVILPMLCNLYSYW 3146  
 QY 3401 WAQGPDNVTPGNGHVTMTVAHNNQLLKNVLUKIKNGIGNENAPMWTTRIATYTOQIIIN 3460





Db 27 ISTLGL---VDRCVVQPEAGDLNPPKFKRCLF-----KLCPMNRYSA-----68  
Qy 1807 HVDQKQLLYAIOSQYMSGFLRGFYD--LLIALHLESHATTWEACKNE-----FVIP 1856  
Db 69 ---QKQFWKAK-----PGANSTTDAVLLNKLH--HAADLEKKQNETENRKLKLTGTVIQ 116  
Qy 1857 LG-----PELKALYEBPDMGHSLRSLOTES-----VRPQWQMTDIASSI 1895  
Db 117 YGNVIQLLHLKSNKYLTNKRPLALLEKNAMRVTLDEAGNEGSWFYIQPFYKLRISIGDSV 176  
Qy 1896 TEISNLYSPYFPLEVAREFVQMALAEAVETNOVHRDVPGGSNENLFLPLIKLVDRLLLV 1955  
Db 177 -----VIGDKVVLNPNVAGQPLHASSH-----QLVDN---P 204  
Qy 1956 GMRDEDEVE---KLLIMTNPETWDPDKGKDBHRKG--LLHMMAEAGAKLQMCYLL 2008  
Db 205 GCNEVNSVNCNTSWKIVLFMK---W-----SNKDDILKGGDVVFLFAEQEKFTCD-- 254  
Qy 2009 QHLNDIQLHRHVEAIIAFAHDFVGLQTDQLRRYTEIKQSDLPASAIAAKTRFRCPPRE 2068  
Db 255 -----EHRKK-----QHVEL-----RTTGRQS-ATSATSKALWEVEVQHD 290  
Qy 2069 -----QNNAILSPKHLEEDKENCPCGEEELIARMEFHTLMAHVSLLHALQEPDAAEN 2121  
Db 291 PCRGGAGYWNLSLFRFKHL-----ATGHYLAAEV-----DPD-----321  
Qy 2122 QEPKAPGAGKLYNIINTVKELEBEAKAIEBPCKTPEE-----KFRKVLIOITVN 2173  
Db 322 -----FEEE---CLEFQPSVDPDQDASRLRNLNAQEKWYLSVS 357  
Qy 2174 WAEESQIET---PKLVREMFSLVROYDAVELIRALEKTYVINAKTKLDVAE--- 2223  
Db 358 VPEGNDISSIFELDPPTLRGGDSLVR--NSVYLRHLCTNTWVHSTNIPIDKEEKPVM 415  
Qy 2224 MWVGLSQR---ALLPVQMSQEBE-----ELMRKRLWK 2253  
Db 416 LKIGTSPLKEDKEAFAIVPSPAERVRLDLDANDASKVLGSIAGKLEKGTITQNERRSVTK 475  
Qy 2254 LVNNHTFF---QHPDLIRV---LVRHENVMVAMNTLGRRAQAQSDAQ 2296  
Db 476 LLEDLVYFTGTNSGQDVLVVFVSKPNREROKUMREQNILKQIFKLQAPPTDCGG-- 533  
Qy 2297 SSQVAEDSKEDTSHEMVAVACRELCYFC---RTGRQONKAMFDFHDFLENSNILL 2351  
Db 534 ---PMLRLEELQORHAPRHICR-LCYVLRHSQDQYRKNQEIYAKQGFQXK-----583  
Qy 2352 SRPSLRGSTPLDVAYSSMLMENTELALAREHYLEKIAVYLSRGLQSNSELVEKGYDLG 2411  
Db 584 -----QIGYDVLAEDTITAL-----LHNNRKLLEKHITAAE 614  
Qy 2412 WDPV-----EGERYLDPLR-FCVWNGESV-----EENANLVI--RLLR 2448  
Db 615 IDTFVSLVRKNRPRFLDYLCLVCSMN-KSPIVTQELICKAVLNPTNADILIEHKLVL 673  
Qy 2449 RPECLGPALRGEGGLLKAI DVANKH-----SERIADRKLREMEQEGDVNFHPLPES 2502  
Db 674 RPEFEGVS---TGENALEAGEBEEVWLFWRDSNKEIRSVSRELAQDAKEG-----Q 723  
Qy 2503 DEDEDYIDTGAAILNPFYCTL-----VDLLGRCAPDAGVIALGNKESLR 2545  
Db 724 KEDRDILSYRYQLNLFARMCLODRQYLAINEISGQLDVLILRCMSDENL-----PYDLR 778  
Qy 2546 A---RAILRSVPLEDQGLVLSRFLTNPAAGEERPKSDMPGSLIPGHKQSVGLFLERV 2602  
Db 779 ASFCRLMLHMDVRDQEQVTFVKA-----RLMSEIPEISAIDDYDSSGTSKD-- 827  
Qy 2603 YGIELOELVYKLE--EAFPLDLRAATMLDRDGCESDMALSNRYIGNSILPLLIKRAY 2660  
Db 828 ---EIKERFAQTMFEVEEYLRDV-VQORPFFSDKEKNKLTFFVNNLARNLI-----YFG 877  
Qy 2661 FYNEAENYASLLDAT-----LHTVYLSKNRMLTKQGEAVSDFLVALTSAMQP 2709  
Db 878 FY---NPSDLLRLTKILLAILDCVHTTIFPISK---MTKGEENKSGSNMRSIHGVE- 929

Qy 2710 SMLLKJLRKLTVDVSKLSEYTTVALRLLTLHYERCACKYGSTGAGQG-AFGASSDEEKRL 2768  
Db 930 ---LMTQVVLRGGGFLPMTMA-----AAPEGNVKKQAEPEKEDIM 966  
Qy 2769 TMLFNSIFDLS-----KMDYEPFLGKALPCLIAIGCALPPDYLSLKNYDDDEFYKGEQ 2823  
Db 967 VMDTKJLIIETILOFILNVRDYR-----ISCLLCI-----FKREFDES-----1004  
Qy 2824 AAGDLNPQVDPQPIINTSSVALNNDLNTIVQKPSHYHDAMASRKIENGWYVGEWSQSD 2883  
Db 1005 -----NSQSESTSS-----GNS 1017  
Qy 2884 KTHPLRKYPMNLNDYKERYKEPVRESLKALLAIGWSEHSEVDIPSNRSMRQSKSG 2943  
Db 1018 QEGSPNVGAL--DFEH-----IEEQAEGI--FGGSEENTPLDLDDH-----G 1056  
Qy 2944 GRPEIVTDSATPDYDYNPHPDVMTNLTLSREMOMAEERLADNAHDIMAKKKKEELVINGG 3003  
Db 1057 CRTFLRLLHLTHMDYPP-----LVSGALQLLFRHSQORQEVLOAFKQVQLVTS-- 1106  
Qy 3004 GIHPQLVPYDLTDEKKKDRERSQEFKLYQYQYKLRPSK-----APOSDEOTTTG 3058  
Db 1107 -----QVDNRYKQIKQDLQRSIVKESLWYKGGPDEPMWGDGASGENEHKKTGEG 1158  
Qy 3059 VAIELRFAYSLLKLIQVIDRATINMKLLKPESTTFSRRSSPKTSTRODIKFFSKAVLPLME 3118  
Db 1159 TS-----KPLKHEST---SSY-----1171  
Qy 3119 KYFSTHRYFATAVATANNUGAASLKEKEMVAALFCKLASLLRSLAALFAGPDVITVRCL 3178  
Db 1172 ---NYRV-----KEIL-----IRLSKLCV 1188  
Qy 3179 QVLVKGIDAKSLVKNCPEFIRTSMLTPFNNAVDDVGHITIMNLQDGKYAHLRGTILKTSTS 3238  
Db 1189 Q-----ESASVRKS-----RKQOORLLRN-----GAH-----1211  
Qy 3239 LGYINGVLLPILTAKFOHLANCEYCADLLDEIQVASYKMLGSLYALGTDSLTHDRKYL 3298  
Db 1212 ---AVVLELQIPY-----EKAEDTKMQEIMRLAHEFLQNF-----1244  
Qy 3299 KTEIRHKPALGCLGAPSTFPVAFLEPHLKNQFSLNRIADHSLEAODIMQKMQC 3358  
Db 1245 -----CAGNOQO---ALLKHINLFLKPGILEAVTMOHI---FMNMFQUC 1284  
Qy 3359 MPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLCLSVLPFWWAGGPDNVPTGNGHYTM 3418  
Db 1285 SEINERV---VOHFV-----HCIE-----THGRNVQY 1308  
Qy 3419 VTAEHMNOCLKNVLKLIKKNIGENAPMWTRIATYVTOQIIINSSEELL-----RDSFLPL 3473  
Db 1309 I--KFLQTIKVAEGKFIK-----QDMVMAELVNSGEDVLVFNDRASFOTL 1354  
Qy 3474 AERVKRTDNM-----FKHGESLGRFTKSTDDTSQVESQIQEDWQLLVRDIYF 3524  
Db 1355 IQMRSERDRMDENSPLMYHILVELL-----AVCTEGKNVYTEIKNSLPLDLDIVRV 1409  
Qy 3525 -----PLLIKYYVDLQBNHMLRNNVPEABEY--NHVABEIPNIWKSQYFLKBEQNFIS 3575  
Db 1410 THEDCIPEVKIAYINF-LNHICYDTEVEEMKEIYTSNHWKULF-----ENFL- 1454  
Qy 3576 ANEDINMVLIMPTATRRVTAVDGTPQGGKKKKKRRDKRDK-DKEYQASLMV-----3628  
Db 1455 ---VD-----ICRACNNTSD-----RGHADSILEKYVTEIVMSIVTTFPSSP 1493  
Qy 3629 ---ACLRLLPVLNLFAGREOELVOHKDRFLKXKSEQDV-----BEFAKQ-LT 3675  
Db 1494 FSDQSTTLQTRQPFVQLQGVFR--VYHC--NMLMPSQKASVESCIKRVLSDVAKSRAIA 1549  
Qy 3676 LPDKID-----PADENSWQHYLYSKLGSKSKSNIT-----VETAENKA 3713  
Db 1550 IPVDLDSQVNNLFLKSHNIVOKTALNWR--LSARNAARRDSVLAAASRDYRNIIERLQDIV 1607





Db 1357 IQMRSEDRMDENSPLMYHILVELL-----AVCTEKNVYTIKCNLSLPLDDIVRVV 1411  
Qy 3525 -----PLIKYVDLQRNHLRNVPABELY--NHVAEIFNTWSKSQVFLKEEQNFIS 3575  
Db 1412 THEDCIPEVKIAYINF-LNHCVYDTEVEMKEIYTSNH-----MWKLVENFLVD----- 1458  
Qy 3576 ANEIDNVIMPTATRRVAVTDTGTPQGGGKKKKHKKDK-DKEVQASLMV----- 3628  
Db 1459 -----ICRACNNTSD-----RKHADSILEKYVTBIVMSVITTFSSP 1495  
Qy 3629 -----ACLKRLPLVGLNLFAGREQLYQHCKDRFLKKMSEQDV-----AEFAKTO-LT 3675  
Db 1496 FSDOSTTLOTROPVFLQLQVFR--VYHC--NWLMPQKASVESCIRVLSDVAKSRAIA 1551  
Qy 3676 LPDKIDPADENSWOHYLYSKLGSKSNITVETAEKAKIIDTVER--IVAMSKVLFLGL 3733  
Db 1552 IPVLDL-----SOVNNLFLK-----SHSIVQKTAMNWLRSARNAARDSVLAASR----- 1596  
Qy 3734 HMIDHPQMSKNVRSVVSIOKRAVIACFR-----QTSLSHL--PRHR----- 3775  
Db 1597 -----DYRNI--IERLQDIVSALEDRLRPLVQAELSVLVDLHRPELLFPENT 1642  
Qy 3776 -----ACNIFARTYVELMEENIGOEVMIEDLTQSPEDAELEKSDVVVEGE-- 3822  
Db 1643 DARRKCSGGFICKLKHITKO--LLEEN--SEKLCIKVLOTLEMTKORGYGEKEAL 1697  
Qy 3823 -----KPDPLTQLVTTFCRGAMTERSALQEDPLYSYAHIAKSCGEEBEEG 3870  
Db 1698 RQVLNRYGVNRPSSRRESLTSPGNG-----PL-----SAGPGKPG 1735  
Qy 3871 GGBEEBGGGEAEDEGRASHEGMEKQKLLFHOARLADRGVAMV--LLHISASKGL 3927  
Db 1736 GG-----GGG-----SGSSMSRGEMLAEV--QCHLDKEGASNLVIDLIMNVSSDR-- 1780  
Qy 3928 PSEVMKTLQILGAGGNIDIQWMLNLH-KDKKDVGF----- 3967  
Db 1781 ---VFHESILALALEGGNTTIOHSPFCRLTEDKSEKFKVYDRMKVAQOEIKATVT 1837  
Qy 3968 --TSIAGLMNSCVLDLDAFERNTKAEGL----- 3994  
Db 1838 VNTDLGNKKKDDVEDRDAPSKKAKEPTTQITEVRDOLLEASAATRKAPTTPREADP 1897  
Qy 3995 -----GVLEGAGEKMKHDAETCA-----LFRFIOLTCEHNLDMQWYLRTOAGNT 4042  
Db 1898 DDHYQPGEGTO-ATADKAKDLENSAVITIMQPIFLRLOLLCENHNRDLQNFRCQ--NNK 1955  
Qy 4043 TTVNVVICTVDYLLRLOES-----IMDFYWHYSSKELIDPAGKANFFKAIGVASQVNT 4096  
Db 1956 TYNVLVCTQLQDCICGSTTGGGLGLGLYNE-----KXVALINQTL 2000  
Qy 4097 LTEVIQPGCTONQQAHLASRLMDAVGGFLFLFHMQDKLSKHSSQVDLLKLLNLQKMI 4156  
Db 2001 LTEYCQGPCHENQNCIA-----THESNGIDIITAI--ILNDIN 2036  
Qy 4157 PMMLSMLEGNVNGTIGKQWVDLIVESASNVELLIKYFDMFLKLDLTSSASFOEIDANN 4216  
Db 2037 P-----LGKRMDLVLKNNASKLL-----LAIMESRHDSENAERILYN- 2076  
Qy 4217 DGWVLPKDFEKKMQOQSYTPEETEFELLACETNHDGKLDYIGFCDRFHPAKBEGFLA 4276  
Db 2077 ---MRPKELVEVI--KXAYMOGEVEF-----EDGENGE-----DGAASP-RVNGHNY 2118  
Qy 4277 VLLTNLSHMPNEPRLARFLTAGSV-----LNFPEPFLGRIBMGSKRIERYFFBIKE 4331  
Db 2119 ILAHLARH---NKELOSLAPGQVGDGEALEFVAKHTAQIEIVLDRMTQEVFPV-- 2173  
Qy 4332 SNISQWEKQI-----KESKAFYFYSIVTEGDKLEAFVNFCEDAIFENTHASGLMAA 4386  
Db 2174 -----PSICEFLTKESKLRIYTT----- 2191  
Qy 4387 SEESVGTKNEASWYMGDDDRAGKDPFRGRGLQSKVDGVATAFSSLSPSNIKAKIAD 4446  
Db 2192 -----TERDEQG-----SKIND 2203

Qy 4447 MQOMPAPAEAVGFKMFYFYLVYGVLVVVRVYIFGVLLGLMRGPOTDEPPPEPTEEEK 4506  
Db 2204 -----FF----- 2205  
Qy 4507 IGO LRHRLLATQSSRHLPALPPADDTGOMQVSAFGLDITKEDNGQIQVKPHEPSTSTPS 4566  
Db 2206 ---LRSE-----DLFNMENW----- 2217  
Qy 4567 SGEEAEVSPDESADHTEQRPPLSIDLLGGEQAKQORMEAAQAAQAAAMSAIEABSKK 4626  
Db 2218 -----QKKLRAQP----- 2225  
Qy 4627 AVOGPAPSALSQVDLSQYTRRAVSFLARNPYNLYVALVLAFCINFVLLF-YKVSTLDGE 4685  
Db 2226 -----VLYWCARNMSFWSSISFNLAVLMLNLLVAFVLPKGVRRG 2264  
Qy 4686 GGGSGGLDIIAGGGSGAGSGGSGGSGEDDDALEVVHIDEDFFYMEHVHVKMAAVL 4745  
Db 2265 TLEPHWSGLLWTG----- 2277  
Qy 4746 HSTVSLAILIGYYHLKVPLAIFKREKEIAFKLEFDGLYIAEQPEDDDDLKSHWDKLVTSK 4805  
Db 2278 -MLISLIGIVG---LPNPHCI-----RAL-----IGSTILRLIFSVG 2310  
Qy 4806 SPFVYWDKPFVKKKVRKAKYSETYDFDSISNMLG-----MEKTSFSAQEEGSKGLIHYIIN 4861  
Db 2311 SQPALF-----LLGAFNVCNKIIF-----LMSFVGN 2336  
Qy 4862 IDWRYQVMKAGVITITNSFLYSLWYFVSFVGMGNF--NNFPPAAHLLDVAVGFKTLRTILQS 4920  
Db 2337 CGTFTGRYRAMVLVDVEFLYHLLYLVICANGLFVHVFFYSLLLLDLVYBEESLLNVIKS 2396  
Qy 4921 VTNGKQLVLTVMLLTIIVYTVIAFNFRKPYV----- 4955  
Db 2397 VTRNGRSIILTAVLALILVYLSIVGLFFKDDFILEVDRLPNETAVPETGESLASEFLF 2456  
Qy 4956 -----QBEDDEVNRCHDMLTCTFVFNLYKGVKAGGIGDEL 4991  
Db 2457 SDVCRVSEGENCSPAPRELVPAEETEODKEHTCTETLLMCIVTVLSHGURSGGVGDVL 2516  
Qy 4992 EPPDGDS-EVYRIIFDISPFFFIIVILLAILLOGLIIDAFAELRDQLESVKEDMESNCFI 5050  
Db 2517 RKESKEPLPAARVYDLEFFFWIIVLNLIIFGVILDTADLRSEKQKKEILKTTCFI 2576  
Qy 5051 CGINKDYFDKVPKGFTHVQREHNLANYMFFLMLINKPDTYTGQBYVNMVYTORCWD 5110  
Db 2577 CGLERDKFNDKTVTFEEHKEEHNMMHYLCFIVLVKVKDSTYTGPEYSVAEMIKERNLD 2636  
Qy 5111 FFP 5113  
Db 2637 WFF 2639

RESULT 8  
US-08-114-555A-8  
; Sequence 8, Application US/08114555A  
; Patent No. 5854392  
; GENERAL INFORMATION:  
; APPLICANT: Manly, Susan P.  
; APPLICANT: Kozlowski, Michael R.  
; APPLICANT: Neve, Rachael L.  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100  
; TITLE OF INVENTION: RECEPTOR (C100-R)  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/114,555A

FILING DATE: 30-AUG-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 6013-115

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-114-555A-8

Query Match 1.3%; Score 336.5; DB 1; Length 240;

Best Local Similarity 34.7%; Pred. No. 2e-18; Indels 47; Gaps 4;

Matches 82; Conservative 37; Mismatches 70; Indels 47; Gaps 4;

Qy 1879 TESVRPQMKMTD-----IAESITEISNLYSPYFPLEVAREFVQMALAEAVETNQVNR 1931

Db 5 TTSLRPPHFPSPCFVAAALPAAGVAEAPARLSPAIPLEALRDKALRMGLGEAVRDGGQAR 64

Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDK 1981

Db 65 DPVGSVBFQFVPLKLVSTLLVMGIFGDEVDVKILKMIPEVFTTEEEEEEEEEEE 124

Qy 1982 EGKDEHRK-----GLLHKMAEAGAKLQMCYLLQHLN 2012

Db 125 EEEDEEEKEDEEEKEDEAEKEEAEPEGEKEDLEEGLLQMKLPESVKLQMCNLLLEYFC 184

Qy 2013 DIQLHRVEAIIAFAHDFVGLDQLDRLRYTEIKOS-DLPSSAAKKTREFCRPPR 2067

Db 185 DQELQHRVESLAFAERYVDKLOANQRSYALLMRAFTMSAAETARRTRFRSPQ 240

#### RESULT 9

US-08-559-397A-14

Sequence 14, Application US/08559397A

Patent No. 6083713

GENERAL INFORMATION:

APPLICANT: Manly, Susan P.

APPLICANT: Kozlowski, Michael R.

APPLICANT: Neve, Rachael L.

TITLE OF INVENTION: CLONING AND EXPRESSION OF

TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/559,397A

FILING DATE: 15-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6013-135  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-559-397A-14

Query Match 1.3%; Score 336.5; DB 2; Length 240;

Best Local Similarity 34.7%; Pred. No. 2e-18;

Matches 82; Conservative 37; Mismatches 70; Indels 47; Gaps 4;

Qy 1879 TESVRPQMKMTD-----IAESITEISNLYSPYFPLEVAREFVQMALAEAVETNQVNR 1931

Db 5 TTSLRPPHFPSPCFVAAALPAAGVAEAPARLSPAIPLEALRDKALRMGLGEAVRDGGQAR 64

Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDK 1981

Db 65 DPVGSVBFQFVPLKLVSTLLVMGIFGDEVDVKILKMIPEVFTTEEEEEEEEEEE 124

Qy 1982 EGKDEHRK-----GLLHKMAEAGAKLQMCYLLQHLN 2012

Db 125 EEEDEEEKEDEEEKEDEAEKEEAEPEGEKEDLEEGLLQMKLPESVKLQMCNLLLEYFC 184

Qy 2013 DIQLHRVEAIIAFAHDFVGLDQLDRLRYTEIKOS-DLPSSAAKKTREFCRPPR 2067

Db 185 DQELQHRVESLAFAERYVDKLOANQRSYALLMRAFTMSAAETARRTRFRSPQ 240

#### RESULT 10

US-08-114-555A-6

Sequence 6, Application US/08114555A

Patent No. 5854392

GENERAL INFORMATION:

APPLICANT: Manly, Susan P.

APPLICANT: Kozlowski, Michael R.

APPLICANT: Neve, Rachael L.

TITLE OF INVENTION: CLONING AND EXPRESSION OF

TITLE OF INVENTION: RECEPTOR (C100-R)

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/114,555A

FILING DATE: 30-AUG-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 6013-115

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 240 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;   MOLECULE TYPE: protein
; US-08-114-555A-6

Query Match      1.2%; Score 334.5; DB 1; Length 240;
Best Local Similarity 35.6%; Pred. No. 3e-18;
Matches 84; Conservative 32; Mismatches 73; Indels 47; Gaps 4;

Qy 1879 TESVRPQMKMTD-----IAESITEISNLSPYFPFLEVARFVQALAEAVETNQVNR 1931
Db 5 TTSLRPPHPSPPCFVAALPAAGAAEAPARLSAIPLEALRDKALRMGLGEAVRDGGQHAR 64

Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDKEGK 1984
Db 65 DPVGASVEFQVPVKLVSTLLVMGIFGDEVDVKQLKMIPEVFTTEEEDEEEDEEE 124

Qy 1985 DEHRK-----GLLHMKMAEGAKLQMCYLLQHLN 2012
Db 125 DEBEKEDEEBETAQEKDEKEEAAEKEEGLEGLLQMKLPESVKLQMCHELLLEYFC 184

Qy 2013 DIQLRHVEAIIAFAHDFVGDLOTDLQRLRY-TEIKQSDLPASAANKTREFRCPPR 2067
Db 185 DQELQHRVESLAAPFAERYVDKLANQRSRYGLLIKAFSMTAAETARRTREFRSPQ 240

RESULT 11
US-08-559-397A-12
; Sequence 12, Application US/08559397A
; Patent No. 6083713
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF
; TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,397A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-135
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 240 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
; US-08-559-397A-12

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Query Match      1.2%; Score 334.5; DB 2; Length 240;
Best Local Similarity 35.6%; Pred. No. 3e-18;
Matches 84; Conservative 32; Mismatches 73; Indels 47; Gaps 4;

Qy 1879 TESVRPQMKMTD-----IAESITEISNLSPYFPFLEVARFVQALAEAVETNQVNR 1931
Db 5 TTSLRPPHPSPPCFVAALPAAGAAEAPARLSAIPLEALRDKALRMGLGEAVRDGGQHAR 64

Qy 1932 DPVGSNENLFLPLIKLVDRLLVGMMDDEVEKLLIMTNPETW-----DPSFDKEGK 1984
Db 65 DPVGASVEFQVPVKLVSTLLVMGIFGDEVDVKQLKMIPEVFTTEEEDEEEDEEE 124

Qy 1985 DEHRK-----GLLHMKMAEGAKLQMCYLLQHLN 2012
Db 125 DEBEKEDEEBETAQEKDEKEEAAEKEEGLEGLLQMKLPESVKLQMCHELLLEYFC 184

Qy 2013 DIQLRHVEAIIAFAHDFVGDLOTDLQRLRY-TEIKQSDLPASAANKTREFRCPPR 2067
Db 185 DQELQHRVESLAAPFAERYVDKLANQRSRYGLLIKAFSMTAAETARRTREFRSPQ 240

RESULT 12
US-09-949-016-8849
; Sequence 8849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8849
; LENGTH: 2262
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8849

Query Match      1.2%; Score 313.5; DB 2; Length 2262;
Best Local Similarity 23.9%; Pred. No. 1.2e-14;
Matches 168; Conservative 110; Mismatches 263; Indels 163; Gaps 36;

Qy 76 LQELVTAAGSETCKGTGSGHRTLL-----YGNAILRLHNSDMYLAC-LSTSSSQDKLAF 129
Db 36 LKKLQHAALAEQ-KQNESENKLLGIVKYSNVLIQHLIKSNKYLTVNKLPALEKNAM 94

Qy 130 DVCLOQHSQGEACWTLHPASKORSEKVRVGDLLVSVATERYLHTTK-----EN--- 182
Db 95 RVSLDA-AGNEGSWFYIHPFWKLRSQDNIVGDKVMPVNAQOPUHASNIELLDNPGC 153

Qy 183 -EVSIVNASFHVTHWSVQPYGTGSRMKYGVY----VFGDVLRFPHGGDECLTIPSTWT 237
Db 154 KEVNAVNCN---TSWKITLF-----MKYSSYREDVLKGGDVRLPHAEQEKFLTCDEYE 204

Qy 238 KCGGQNI-----VVEGGSVMSQARSRLWLELA-RTKAGGFINWYHPMRIRHTTTGYLG 292
Db 205 KK--QHIFLRTTLRQSATSATSKALWEIEVHHDDPCRGAGQGMNSLFRPKHLATGNLYA 262

Qy 293 V-----NDONE-----LY-LVS-----REEATTAS 311
Db 263 AELNPDYRDAQNEGKVRGCVPTSKKQKQAGKIMTTLVSVPHGNDIASLFDATLTQ 322

Qy 312 CAFCLRQEKDDQKQVLEDKLEVIGAPIIKYGDSTVIVQHSSETGLMWSYKSY-----ETKK 367

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Db 323 RADCLVPR-----NSYVRLRHLCNTWTSTSTIPIDTDEER 358
Qy 368 KGVGKV-----EKKQALHEEGKMDGLDFSRQOEESRTARVIRKCSSLFTFKFINGLE 421
Db 359 PVMLKIGTCQTKEDKEAFIVSVPUSEVRDLDFDANKVKVLAATTVKLE-----NG-- 409
Qy 422 TLQENRRHSMPFASVNLGEMVCLBDLINYFAQ--PDEMEHEE-----KONKFRALNRQD 476
Db 410 TITQNERF-----VTKLLEDLFFVADVNNQGEVLDVVTXPN-----RERQK 454
Qy 477 LPOBEGILN-----ILEADKINVTISQGLAGFL--AGDESGOSWEMISGYLYQLLALAIK 532
Db 455 LMREQNIIAQQVGIILKAPFEK--AGEGSMRLLEDGLDQRYAPYKMYMLRLCYRVL----- 507
Qy 533 GNHTNCAQFANSNRLNWLFSRLGSOASGEGTGM--DVLHCVLIDSPALNM--MRDEHIK 589
Db 508 -RHSQDVRKQEQYIAKNCVWQSQI-----GVDILAEDTITALLHNNRKLKHEKHTAKEIE 563
Qy 590 VIISLEKHGRDPKVDLCSLCVNGVAVRSSQNNICDYLL--PGK-NLLQTLALVDHVS 647
Db 564 TFSVLLRN--REPRDLVSLDLCVSNTTAIPVTQELICKFMLS PGNADILIQTKVVSQA 622
Qy 648 S--VRPNFVGRVGSAYVRKYFVETMDHIEKTHMMPHLRIG 689
Db 623 DNPMESSILSDIDDEEVWLYMIDSNKEPHGKAIRHLAQEAKEG 666

RESULT 13
US-09-949-016-6507
; Sequence 6507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6507
; LENGTH: 3259
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6507

Query Match 1.1%; Score 308; DB 2; Length 3259;
Best Local Similarity 18.7%; Pred. No. 6.8e-14;
Matches 637; Conservative 557; Mismatches 1216; Indels 988; Gaps 171;

Qy 1283 NTFET-----MKAWEFURLSLPVICHN-----EFTDEAKA--RRWEIKDROOI 1327
Db 308 NTVTEREESKILLEKMELEVAERKLSP--HNLQEMHLLLEQFEQAGQAQAELESRYSA 365
Qy 1328 LMW--EAVEAQPAAHIDQIMRSG-----FTMNDIKGLHYEDNOEELPSS--KMKRLPS 1376
Db 366 LEQKHAEMEETSHLSLQKTGOELQACDALKQNKSKLQDKNNEAVQSAQTQQLED 425
Qy 1377 RPRKGSMTGRVTIONYNLPQGVNGHRSTRSEAMAK--YDLGAQGLTPDDPKDKRGSR 1435
Db 426 QIQQSK-----EISOFLNRLPLQ--QHETASQTSFPDVYNEGTQAVTEENIASLQKRV 477
Qy 1436 PKFPRSKGESSDRAKSRKSTPDPFSDTVEPSRGARRPNPQIKVSOANORYNGMAR 1495
Db 478 -----VELENEKGA----- 486
Qy 1496 PSRTNLYGSOVLNWPQDRKQMTSTL--AQSATETVGNEIFDAECLKLINEFYGV 1553
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Db 487 -----LLSSLELE-ELKAENEKLSQITLLEAQNRTGEADREYSEISIVDIANKRSSA 540
Qy 1554 RIYPGDPTHYVIGWVITQYHLHSDKDNQSKVTKSSVLIITDYDRVVENVNQRSCYM-- 1610
Db 541 E-BSGQD-----VLENTFSQ--KHKELSVLLLE-----MKEAQEEATFLKQ 579
Qy 1611 ---VRADELYNEVMAEATAKASQCMFICGSVDSTSGVSFTCBGKDTSPFKMEP--BTK 1666
Db 580 LOGKRAEADHEVLDQXEMK--QMEGEGI-----APIKMKVLEDTGQDFPLMPNEES 630
Qy 1667 LPPAIFVEATSKETILOELGRSATSLPLS---AAVLPTSDGH-----VTPQP----- 1711
Db 631 SLPAVEKEQASTE-----HQSRTSSEISLNDAGVELKSTKQDQKSLSAVPDQGCHQD 684
Qy 1712 --PRLKVQCLKP-----HQAARVPNQSLOVHALK----- 1738
Db 685 ELERLKSOILELNFHKAQEIYKNDLDEKAEISNLNQLIEEFKQKADNNSAFTALUSE 744
Qy 1739 -----LSDIRGWSMLCE--DAVSMALAHIPBED--RCIDILEPIEMDKLLSFHSHTLTLY 1789
Db 745 ERDQLLSQVKELSMVTELRAQVKOLEMNLAEARQRRLDYESTAHDNLLTEQIHSLSIE 804
Qy 1790 AALCYQSNYRAAHALCTHVDQKQLLYAIQS---QYMSGPLRQGFYDILLIAL-----HLSEH 1842
Db 805 A-----KSKDVKIEVLQNELDDVQLQFSQSTLIIRSLOSQLOKQSEVLEGAERVRHISK 860
Qy 1843 ATTMEACKNEFVPLGPPELKALYEEDPMGHGHSLSIQTESVRPQMKMTDIAESITE-ISNL 1901
Db 861 VEELSQALSQKELEITKMDQLLEKK---RDVETLQOTIEKQDQQTVEISFMTBKMVQL 917
Qy 1902 YSPYFPLEVAREFVWQAL-----AEAVETNOVHNRDPV--GGSNENLFLPLIKLDVRLLLV 1955
Db 918 NEEKFSLGVEIKTLKEQLNLLSRAEAKKEQVEEDNEVSSGLKQN-----YDEMSPA 969
Qy 1956 GMMRDEDEVKLLIMTNPETWDPSPD---KEGKBHRKGLLHMAAGAKLQWYLLQHLN 2012
Db 970 GOISKEELOH-----EPDLLKKEQQRKR-----LQAALINRKEELLQVRS 1010
Qy 2013 DIQ-----LRHREAITAFADHFVGDLOTQ--QLRRYTEIKQSDLPASAQAKTFRFCPP 2066
Db 1011 KLEELANLKDSEKKEIPLSETERGEVEEDKENKEYSE-----KCVTSKCQIEIYL 1062
Qy 2067 REOMN-AILSPKLEEDKENCPCGEELIARMNPFHDTLMAHVSILHAHQEPDAENQ--- 2122
Db 1063 KQTISEKEVELQHRKOLEEKLAAEQFQALVKQNNQTLQDKTNQIDLLQAEISENQAI 1122
Qy 2123 -----BPEAKPG---AFGKLYNIINT-----VKELBEEAKAIEBPCKTPEEKR 2164
Db 1123 QKLITSNTDASDGSVALVKETVVISPPCTGSSEHWKPELBKILALEK-EKEQLQKKLQ 1181
Qy 2165 KVLJ--QTIWNWABESQ---IETPKLVREMFSLVRQYDA-----VGEILRALEKTIV 2212
Db 1182 EALTSRAILKKAQEKERHLREELKQKQDDYRNLQEQDEOSKENENIGDQLRQJ--- 1237
Qy 2213 INAKTLDVAMWVGLSQIRALLPVQMSQEEEL-----MRKRLWLKLVNHHFTFQHPDL 2266
Db 1238 IQVRESID-----GKLP---STDQOESCSSTPGLEELPFKATEQH-----HTQP 1278
Qy 2267 IRVLRV-----HENVMVMNTLGRRAQASQPSQPVVAEDSKEDKTSHEMVVACC 2319
Db 1279 VLESNLCDFWPSHSEDASALQGGTSVAQIKAL--KEIEAEKVELEKLVKSVSTTSELT--- 1333
Qy 2320 RPLCYFCTGRONQKAMDFDHFDFLLENNILLSRPSLRG-STPLDVAVSSL---MENTEL 2375
Db 1334 -----KKSEVFQLOEQINKQGLETSKTVSHEAEVHAESLQQLLESSQL 1379
Qy 2376 ALALREHYLEKIAVYLSRCGLQSNSELVEKGPDLGWDPEGERYLDLFLFCVWVNGESV 2435
Db 1380 QIAGLEHURE-----LQPKLDELQKLSKKEEDVS-----YLSGQLS 1416
Qy 2436 BENANLV-IRLLIRPECLGPALRGEGLLKAI-----VDANKMSEIRADRR-KLREME 2488
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Db 1417 EKEAALTKIQTEII-----EQEDLIKALHTQLEWQAKEDHERIKQLOVELCEMK 1465  
Qy 2489 QEGDWNFSHPUPESDEDEYI-----DTGAAILNFYCTVLVDLGRCAPDAGVIALGKNE 2542  
Db 1466 QK-----PEBIEESRAKQOIQRKLQAALI-----SRKEALKENK 1500  
Qy 2543 SLR-----ARAILRSLV-PLEDLOGVLSLRFTLNNPAAG-----ERPCK--SDMPGSLI 2588  
Db 1501 SLOBELSLARGTIERLTKSLADVESQVSAQNKQKDTVLGRLLAQLEBERDKLITEDRSLL 1560  
Qy 2589 PGHK-----QSVGLFPLERVYGIETQELFYKLLEBAFLPDLRRAATMLDRNDGCESDMALSM 2643  
Db 1561 ENQSLSSCESLKLAEGL--TEUKE--KLVKE--IESLKSSKIAESTEWEQKHKELOK 1613  
Qy 2644 NRYIGNSILPLIKHAYPYNBAENYASLLDNLHTVYRL-----SKNRLMTKGOREAV 2696  
Db 1614 EYEI-----LQSVENVNNEARIQHVAEVRQEQELVGLRSTANKETEKOLQEA 1667  
Qy 2697 SDFLVALTSANQ---PSMLLKLLR-----KLTVDV-----SKLSEYTVV--A 2733  
Db 1668 EQEMEEMKEKMRKFAKQKQKILEBEENDRLRAEVRHPAGDTAKCEMETLLSNASMKEE 1727  
Qy 2734 LRLTLHYERCAKYVSTGAGOGAFGASSDEKRLTNMLFSNI-----FDSLSKMDYE-- 2786  
Db 1728 LERVMEYETLUSKFPQSLMSEKDSL---SEEVQDLKHQIEDNVSKQANLEATEKHNDQTN 1784  
Qy 2787 -PELFGKALP-----CLIAIGCALPPDYSLSKNYD--DEFYG----- 2820  
Db 1785 VTEEGTQISPGETEEOQSLSMSTRPTCSVPSSAKSANPAVSKDFSSHDEINNYLOQIDQ 1844  
Qy 2821 -KEQAAGDLPQVDPQPIINTSSVALANDLNTIVQKSEHYHDWASRKENGWVYEGW 2879  
Db 1845 LKERIAGLEEKQNKKE-----FSQTLNEKNTLLSQIS-----TKOG----- 1882  
Qy 2880 SDSOKTHPRLPYNMLNDYERKYEPVRESLKALLAIGMSVERSEVDIPSNRRSMRQ 2939  
Db 1883 -ELKMLQEEVTKMMLN-----QQIOEELSRVTKLKEAEBEKDDEERLMNQLAEL 1933  
Qy 2940 SKSGRRPEIIVTDSATPPDYNPHVPDMTNLTLSREMOMARLADNAHDIAWKKKEELY 2999  
Db 1934 NSGIGNYQDVTDA-----QIKVELLESEMKNLKKVSE-----LEBEKQQLV 1976  
Qy 3000 TN-----GGGIHPQLVPYDILLTDKEK-----KKDRERSOEFL 3031  
Db 1977 KEKTKVESEIRKEYLEKIQGAQKPEGNKSHAKEL--QELLKEKQOEKVLQKDCIRYQEKI 2035  
Qy 3032 KYLOVQGYKLRPSKAPQSDTEQTTGVA-----IELRPAYSILLEKLIQYIDRAT 3081  
Db 2036 SALERTVVALEFVQTESQKDLLEITKENLAQAVEHRKKAQAEALASFVKVLLDDTQSEAAARVL 2095  
Qy 3082 I--NMKLLK--PSTTFSRRSSPKTSTRDIKFFSKAVLPIMEKYFSTHRNYFIATATANNV 3138  
Db 2096 ADNLKLLKELQSNKESVKQMKQKDEDL-----RRLEQAEKHE----- 2134  
Qy 3139 GAASLSEKEMVAALFCKLASLLRLAALFAGDPDVRITVRCLOVLV--KGIDAKSLVKNCP 3196  
Db 2135 ----LKEKNQOE---KLDALRREKV-----HLEETIGEIQVTLNKKDKVEQQLOENLDS 2182  
Qy 3197 FIRTSMLTF---PNNVADDVGHIT-----MNLQDGKYAHLRTHL 3233  
Db 2183 TV--TQLAAFTKMSLQDRLDRVRIDEAKKWERKESDAIQSKEEIRLKEKNCVSLKQDLR 2241  
Qy 3234 KTSTSLGYINGVLLPILTAKEPDH-----LANCEYG--ADLLLDEIQVASYKMLGS---- 3281  
Db 2242 QMS-----IHMEELKINISRLHDKQIWEKSAQTEVQLQKQVCDTLQENKELLSQLEET 2296  
Qy 3282 --LYALGTD--ASLTHDKYIKTE-----IERHKPALGSCIGAF-----SSTFPV 3322  
Db 2297 RHLVHSSQNEALAKLESLSKLDQTLDSNLEKCEKQKGNLEGIIRQOEADIQNSKFSY 2356  
Qy 3323 AFLPHELNKHNQFSLNRIADH--SLEAQDINQKQECQMPTLETITLGEVDQVQESDKTYNE 3381  
Db 2357 EQLETDLQASRE--LTSRLHEINNKQKILISLSGKEEAIOVAIELRQ--QHDKEIKE 2412

Qy 3382 APHIIDVLPLLCSYLPFWWAQGPDNVPTGGNHVTVMTVAEHNOLLKNVLIKKKNIGN 3441  
Db 2413 LENLSS-----QEEENIVLEEENKAV---DKTNQMLE--TLKTIKK----- 2450  
Qy 3442 ENAPMWTIRIATYQOI--IINSSEELLRDSFLPLAER---VRKRTDNMFHK-----E 3488  
Db 2451 ENIQQAQLDSFVKSSSLONDRDRIVGD--YQOLEERHLSIILEKQOLIOEAAENNKLK 2509  
Qy 3489 ESIRGFIKSTDDTSQVES-----QIOEDWOLLVRDIYFSFYPLLIKYVDLQRNHLWRN 3541  
Db 2510 EETRIG--LRSHMDLNSENAKLDAELIQYREDLQOVITIKDSQKQKLE--VLOQONKELEN 2567  
Qy 3542 NVPEAEELYNHVAEINFINWSKQYFLKEEQNFISANEIDNMVLMPTATRVTAVDGTGP 3601  
Db 2568 KYAKLEBKLESBEANEDLRRSFNAQOEKQDLS--KEIBSKVSIQSOLTQVATLQEGT 2626  
Qy 3602 QGGGKKKKHRDKRDKKEVQ--ASIMVACLKRLLPVGLNLPAGREQELVQHKORFLK 3659  
Db 2627 LG-----LYHAQLKVKEBEVHRLSALFSSQKRI-----AELEELV--CVQK--- 2667  
Qy 3660 KMSEQDVAEFQTLTPDKIDPADEMSQHYLYSKLGSKSNIIVTETAENK--AKIID 3718  
Db 2668 -----EAAKKVGEIEDKL--KKELKHLHDGAGIMRNET-----ETAERVAELARD 2711  
Qy 3719 TVB--RIVAMSKVLFGHLMIDHPQMKVYRVSIVSIQKR-----AVI 3760  
Db 2712 LVMEQKLLMVTENKGL-----TAIQSFGSMSLQNSRDHANEELDELKRYKIDASL 2765  
Qy 3761 ACFRQTSLSLPRHACNTFARTYBELWLEEN-----IGOEVMIED-----LTQSFE 3808  
Db 2766 KELAQLKEQGLNRDALLSETAFPMNSTEENSLSHLEKLNQQLLSKDLQLHLSQLE 2825  
Qy 3809 DA-----ELKXSDVVVEBEK-----PDPLT-----QLVTTFCRG 3837  
Db 2826 DSYNVQVSFSKAWASLQNERDHLWBLEKPRKSEEGKQSAAPSTSPAEBVQSLKKAMSS 2885  
Qy 3838 AMTERSGALQES--DPLVSYNAHIIAKSCGEBEEEGGEEGGAEEADEGRA--SIHEQE 3895  
Db 2886 LQNDRLLLKELKNLOOQVLOI-----NOBITELHPLKAO---LQEQDKTKAFQIMQEE 2937  
Qy 3896 MEKQKLLF---HOARLA-----DRGVAEMVLLHISAKGLPSEMVMKTLQIGISILR 3944  
Db 2938 LROENLSWQHLEHQLRMEKSSWEIHERMKEQYLMALS-----DKOQLSHLQNLIRELR 2992  
Qy 3945 GGNIDIQMGMLNHLKDKXDVGFFTSIA--GLMNSCVSLDLDAPERNTKAEBGLVGLGAA 4002  
Db 2993 SSSSQTOPLKVQY---QROASPETSASPDGSONLVYETELLRTQLNDSL----- 3038  
Qy 4003 GEKNMHDABFTCALFRPIQLTCEGHNLDQNYLRTQAGNTTVVNVICTVDYLLRLOESI 4062  
Db 3039 --KEIHQKE-----LRIQQL-----NSNFSQLLEEK-----NTLSIQLCDTSQSURENQ-- 3081  
Qy 4063 MDPYWHYSS-----KELIDPAGKANFFKAIGVASQVNTLI-----TEVIQGPC 4105  
Db 3082 -----HYGDLNHCVALEKQVQEL--QAGPLNIDVAPG--APOEKNGVHRKSDPEELREP- 3132  
Qy 4106 TONQQAALAHSRLDVAVGGFLFSSHQDKLSKSHSSQVDLLKELINLQKQK---IPMMLSM 4162  
Db 3133 ---QQS-----FSEAQQQLCNTRQEVNELRKLLEERDQVAAENALSV 3173  
Qy 4163 LEGNV-----VNGTIGKQMVDTLVESASN 4186  
Db 3174 AEEQIRRLHESEWDSRTPPIIGSCGTQEQEALLIDLTSN 3211

## RESULT 14

US-09-710-279-2964  
; Sequence 2964, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS





Db 2755 QKVQLANQALNDAMKLLDALTGNDAIKQTSYINEDTSQQVNF-----DEYDTR 2804  
Qy 2512 GAAIL-----NFVCTVLVLLGRCAPDAGVJALGKNESLRARILRSUPLVEDLOGVLSL 2565  
Db 2805 GKNIVAEQTNPMSPNTINTI-----ADKITEAKN-----DLHGVOQL 2842  
Qy 2566 RFTLNNPAAGEERPKSDMPGSLIPGHQSGVLFLERVYGIETQELFYKLLBEEA-FLPDLR 2624  
Db 2843 -----EQAQOQSINTINQMTGLNAQKEQLN---OEIQOTOTRSEHVQVINKAQLNDSM 2894  
Qy 2625 AATMLDRDNGCESDUALS-MNRYIGN-----SILPLLIKHAIFY 2662  
Db 2895 NTLRQSIDHEVQKTSYININETVGNQTYNNAVDVRVKQIINQTSNTPMPLVERA--- 2951  
Qy 2663 NEAENYASLLDATLHTVVRYSKNR-----MLTGOREAVSDPLVALTSAMQPSM 2711  
Db 2952 --TSNVKTSKA-LHGERELNDKNKSTFAVNHLDNLNAQKEALTHEIEQATVTSQVNN 3008  
Qy 2712 LLKLLRLTVDVSKLSEYTTVALRLTLHYERCAKYGSGAGOGAFGASSDEEKRLTMM 2771  
Db 3009 IYNKAKALNNDMKLKOIV-----AQODNVQ----- 3035  
Qy 2772 LFSNIFDSLKWDEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDP 2831  
Db 3036 --SNY-----INEDSTPQWYNDTINHAQSIIDQVANP 3067  
Qy 2832 QYDPOPINTSVANLNDLNTVQKSEHYHDASRKIENGWYVGEQMSQKTHPLKP 2891  
Db 3068 TMSHDEIEN---AINNIKHAINALDGEH-----KLQQA-----KENANLL- 3104  
Qy 2892 YNMLND-----YEKERYKEPVRESLKALLAIGHSVEHSEVDIPSNRSMRQ 2939  
Db 3105 INSLNDLWAPORDAINRLVNEAQTRKVAEQLOQSAQALNDAMKHLRSI---QNOSVRQE 3162  
Qy 2940 SKSGRPPEIYDTSATPDYNPHPVDMTNLTLSREMONMAERLADNAHDIAWKKKEELV 2999  
Db 3163 SK-----YINASDAKQYN-HAV-----REVENINEQ----- 3190  
Qy 3000 TNGGGHPQLVPYDLLTKKKDRERSQEFLKYLOVGYKHLRPSKAPOSDTEQTGTG 3059  
Db 3191 -----HPTL-----DKE----- 3197  
Qy 3060 AIELFAYSLLLEKLIQYIDRATINM---KLIKPTSTFRSSFKSTREDIKFESKAVLPL 3116  
Db 3198 -----IIKQTDVANOANDLGVELLDDADQKNAHOS-----IPT 3232  
Qy 3117 MEKYFSTHRNYFIATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAGPDPVITVR 3176  
Db 3233 LMHLNQAQON---ALNEKINN-----AVTRAKVAALIGQAKILDH 3269  
Qy 3177 CLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITIMNLQDGKYAHLRGTHLKTS 3236  
Db 3270 AMENLEESIKDKEQVKQSSNYI-----NEDPDVQETVYNAVD-----HVTE- 3310  
Qy 3237 TSLGYINGVLLPIITAK-FDLHANCEYCADLLDEIQVASYKMLG--SLYALGTDSALTH 3293  
Db 3311 ----ILNQTVNPTLSIEDIEHAIN-----EVNQAKQLRGKQLYQT-IDLA--- 3352  
Qy 3294 DRKYLKTEIERHKPALGSCIGAFSPSTPPVAFLEPHLNKHQFSLNRI---ADHSLEAQDI 3351  
Db 3353 DRKLSKLD-----DLTSQSSSISNQIYAKTRTEVAQA 3386  
Qy 3352 MQK---MEQCMPLETILGEVDQFVESDK-----TYNEAPHIIDVVLPLLCYSYP 3398  
Db 3387 IEKAKSLNHAMKALNKLYKNADKVLDSRSRFINEDQPEKEAYQQAINHVDISI----- 3438  
Qy 3399 FWAQGPNDVPTGCHVNT---MVTAE-----HMNQLLKNVL 3432  
Db 3439 --HRQTNPMDPTVINSITHELETAQNHLHGDKLAHAKODAAKVINGLHTLNVQAOREVM 3496  
Qy 3433 -----KLIKKNTGNENA-----PMMTRIATYQOI--I 3458  
Db 3497 INTWNTATREKVAKNLNDNAQALDKAMETLQOVVAHKNNILNDSKYLNEDSKYQQOYDVR 3556

Qy 3459 INSSEELLRDSFLPLAE--RVRKRTONMFHKEESLRGFIKSTDDTSQVESQIQEDWQLL 3516  
Db 3557 IADAEQLLNQTTPTTLEPYKVDIVKONVLANEKILFGAEKLSYDKSNAND----- 3606  
Qy 3517 VRDIYSFYPLLIKVDLQRNHLRNNVPEA-BELYNHVAEIFNIWSKSOYFLKEE--QNF 3573  
Db 3607 -----EIKHMYLNNAKQSIKDMISHAA-----LRETVKQLL 3639  
Qy 3574 ISANEIDNMVYLIMPTATRRV---TAVTDGTPQGGKKKK---KHKRDKDKDKEVOAS 3625  
Db 3640 QOAKTILDEAMKSLDQTVVITDTLTPNYTEASEDKKEKVDQTVSHAQAIIDKINGSNVS 3699  
Qy 3626 L--MVACLKRLLPVGLNLPAG-REQELVQHCORF-----LKMSQODVAEPAKTQTLTP 3677  
Db 3700 LDQVRQALEQLOQASLNDGDQREBEAKVHANOTIDOLTHLSLQOQTAKESVKNATKLE 3759  
Qy 3678 DKIDPADEMSQWLYLSKLSGSKSNITVETAENKAKIIDTVERIVAMSKVLFGLHMID 3737  
Db 3760 EATASNALALNKVWKLEQFINHADSIENSNYRQADD--KIIAYDDAL-----E 3810  
Qy 3738 HPQMSKNVYRSVSVIORKRAVIACFR-QTSLHSLPRHRACNIFARTYVELWLEENIGQ 3796  
Db 3811 HGQIOKS--NATONEAKALQOLINAETSLNGFERLHARPRALEYIKS-LEKINNAQ 3866  
Qy 3797 EVMIED-LTQSPEDAELKKSDVVEGE-----K 3823  
Db 3867 KSALEDKVTQSHDLELE--HLVNEGTLNLDINGELANAIVNNVYPTKASINVINADNLR 3924  
Qy 3824 PDPLTQLTFTFCRGAMTERSGALQEDPLVMSYAHIIAKSCGEEEGGEGGEGGAEAA 3883  
Db 3925 KDNFTQAINN-ARDALNKTCQGNLDFNAIDTPKDDIFKT---KDALNGIERLTAASKA 3979  
Qy 3884 E-----DEGRASIHQEMEKQKLLFHQARLADRGV-----AE 3915  
Db 3980 EKLIDSLKFINKAQFTHANDEIMVNTNSIAQLSRVNAQFPLNDAMKSLRDLNNAQPPVQ 4039  
Qy 3916 MWLLHLSASGLPSEM--VMKTLQLOGISILRGNID-IQM-GMLNHLKDKKQDVFFTSIA 3971  
Db 4040 ASSNYINSDLEDLQOQFDHALSNARKVLAKENGKNLDEIQIEGLQKQVIEDTKDA----- 4092  
Qy 3972 GLMNSCVLDDLAFAFENTRAEGLGV-----GLEGAAGEKNMHDAEFTCALFFIQ 4021  
Db 4093 -----LNGIQRLSKAKAKAIQYVQSLSYINDAQRIAESNIHNSDDLSLANTLS 4142  
Qy 4022 LTCEGHND--WQNYLRTQAGNTTV--NVVICTVDYLLRLQ-ESIMDFWVHYSKELID 4076  
Db 4143 ---KASDLDNAMKDLRDTLESNSTSVPSVNYINADKNLQIBFDEALQOASATSKTSEN 4199  
Qy 4077 PAGKANFFKAIQVASQVFNLTLEVIQGPCTONQOALAHSLDWDVGGFLFLFSHMOKLS 4136  
Db 4200 P---ATIEEVLGLSQAIYDTKNAL-----NGEORLA-----T 4228  
Qy 4137 KHSQVDDLKELLNLOKDMIPMLMLEG--NVVNGTIGQMVDTLTVESASNVLELILKYF 4194  
Db 4229 EKSQDKLILKGLKDLNK-----AQLEDVTNKVNS-----ANTLTLSQLQSTSLKN 4275  
Qy 4195 DMFLKLKD-----LTSASFOEIDANNQDGVLPKDFKEMEQKQSYTPEBIEFLFLLAC 4246  
Db 4276 DKMKLLRDLKTLVNPVKASLNYRNADYN---LKRQFNKALKEAK----- 4317  
Qy 4247 CETNHGKLDYIGFCORFHEPAKEIGFNLA---LLT---NLSEHMPNEPLAR--- 4294  
Db 4318 -----GVLN-----KNSGTNVNINDIOHLLTQIDNAKQOLNGERLKEHQK 4359  
Qy 4295 ---FLETAGSVLNYFPFLGRIBIMGSKRIERYPEIKESNIEQWPKQ-IKESKRAFF 4350  
Db 4360 SEVFIILKELDILNNAQK-AAINQIRASKDI-KLIINQVDNALIELNDAMQGLKE----- 4411  
Qy 4351 YSIVTEGGDKKLEAFVNFCEDAIFEMTHASGLMAAASESVGGTKOREASYM--YMGDDD 4408  
Db 4412 HVAQLTATTKDNIE-YLNADDEDLKIQVDYAINLANNVLDKENGT-NKDANIIGMIQNMD 4469





GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: October 6, 2006, 23:58:04 ; Search time 465 Seconds  
(without alignments)

5108.314 Million cell updates/sec

Title: US-10-668-767-128

Perfect score: 26800

Sequence: 1 MAEAGGASEQDDVSFLRTE.....WDFPPVGDGRKQYEDLMGE 5128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pap.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pap.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pap.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26800	100.0	5128	4	US-10-668-767-128
2	26716	99.7	5134	4	US-10-668-767-130
3	26644	99.4	5142	4	US-10-668-767-144
4	26506	98.9	5100	4	US-10-668-767-146
5	26469	98.8	5142	4	US-10-668-767-2
6	21630	80.7	5127	4	US-10-668-767-8
7	21403	79.9	5127	4	US-10-668-767-122
8	21376	79.8	5113	4	US-10-668-767-121
9	21360	79.7	5127	4	US-10-668-767-120
10	21326	79.6	5109	4	US-10-668-767-10
11	21270.5	79.4	5107	6	US-11-097-143-22563
12	21234.5	79.2	5112	4	US-10-668-767-125
13	21218.5	79.2	5126	4	US-10-668-767-56
14	21218.5	79.2	5126	4	US-10-668-767-124
15	21191.5	79.1	5112	4	US-10-668-767-126
16	21175.5	79.0	5126	4	US-10-668-767-123
17	21046	78.5	5104	4	US-10-668-767-6
18	20932.5	78.1	5101	4	US-10-668-767-4
19	20422.5	76.2	4868	4	US-10-668-767-57
20	12129	45.3	5317	4	US-10-668-767-59
21	11938.5	44.5	5071	4	US-10-668-767-58
22	11868	44.3	4967	4	US-10-668-767-61
23	11840	44.2	4967	4	US-10-668-767-62
24	11561	43.1	5107	4	US-10-369-493-6377
25	11453.5	42.7	4868	6	US-11-044-111-24
26	11407.5	42.6	4870	4	US-10-764-425-144
27					Sequence 144, App

28	11347.5	42.3	5038	5	US-10-723-860-1310	Sequence 1310, Ap
29	11347.5	42.3	5038	5	US-10-756-149-5039	Sequence 5039, Ap
30	11347.5	42.3	5081	5	US-10-450-763-35328	Sequence 35328, A
31	11338.5	42.3	5081	4	US-10-276-1774-1850	Sequence 1850, Ap
32	11325.5	42.3	5032	4	US-10-408-765A-26	Sequence 26, Appl
33	11325	42.3	4899	5	US-10-450-763-42673	Sequence 42673, A
34	11222	41.9	4934	5	US-10-450-763-53705	Sequence 53705, A
35	10863.5	40.5	4767	4	US-10-276-774-1902	Sequence 1902, Ap
36	8109	30.3	3647	4	US-10-408-765A-2436	Sequence 2436, Ap
37	7530.5	28.1	3375	6	US-11-044-111-23	Sequence 23, Appl
38	4953	18.5	2055	4	US-10-276-774-1795	Sequence 1795, Ap
39	2709.5	10.1	1056	6	US-11-044-111-22	Sequence 22, Appl
40	1146.5	4.3	1425	5	US-10-450-763-53703	Sequence 53703, A
41	847	3.2	249	5	US-10-784-004-338	Sequence 338, App
42	730.5	2.7	323	5	US-10-450-763-35329	Sequence 35329, A
43	723.5	2.7	616	5	US-10-450-763-53704	Sequence 53704, A
44	712	2.7	1232	5	US-10-450-763-34060	Sequence 34060, A
45	698.5	2.6	599	5	US-10-450-763-53702	Sequence 53702, A

## ALIGNMENTS

RESULT 1  
US-10-668-767-128  
; Sequence 128, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Linong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; PRIOR FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 128  
; LENGTH: 5128  
; TYPE: PRT  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; OTHER INFORMATION: pXL-Hv7  
US-10-668-767-128

Query Match	100.0%	Score	26800;	DB	4;	Length	5128;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	5128;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MAEAGGASEQDDVSFLRTE	DMVCLSC	TATGERVCLAAEGFGRHCF	LENADKNIP	PD	60
Db	1	MAEAGGASEQDDVSFLRTE	DMVCLSC	TATGERVCLAAEGFGRHCF	LENADKNIP	PD	60
QY	61	SQCVPVIRQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLAC	LST	120			
Db	61	SQCVPVIRQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLAC	LST	120			
QY	121	SSSQDKLAFDVLGLOQHSQGEACWMTLHPASKORSEKVRVGGDDILVSVATERV	LHTTK	180			
Db	121	SSSQDKLAFDVLGLOQHSQGEACWMTLHPASKORSEKVRVGGDDILVSVATERV	LHTTK	180			
QY	181	ENEVSIVNASHVTHWSVQPTGTISRMYGYVGGVLPFFHGGDECLTIPSTWT	KDG	240			
Db	181	ENEVSIVNASHVTHWSVQPTGTISRMYGYVGGVLPFFHGGDECLTIPSTWT	KDG	240			

Qy	241	QONIVVYEGGVSQARSWLRLRLARTKWAAGFFINWYHPMRIRHITTTGRYLGVDNQNELY	300
Db	241	QONIVVYEGGVSQARSWLRLRLARTKWAAGFFINWYHPMRIRHITTTGRYLGVDNQNELY	300
Qy	301	LVSREEATTASCAFCLRQEKDDQKQVLEDKLEVIGAPIIKYIGDSTVIQVHSETGLWLSY	360
Db	301	LVSREEATTASCAFCLRQEKDDQKQVLEDKLEVIGAPIIKYIGDSTVIQVHSETGLWLSY	360
Qy	361	KSJETKKGVCKVBEKQAILHEEGKMDGLDFRSQBEESSTARVIRKCSLSLTFKFINGL	420
Db	361	KSJETKKGVCKVBEKQAILHEEGKMDGLDFRSQBEESSTARVIRKCSLSLTFKFINGL	420
Qy	421	ETLOENRRHSFFASVNLGEMWMCLEDLINVFAQPDDEMEHEEKONFRALRNRQDLFOE	480
Db	421	ETLOENRRHSFFASVNLGEMWMCLEDLINVFAQPDDEMEHEEKONFRALRNRQDLFOE	480
Qy	481	EGILNLNLEAIDKINVTISQGFAGLAGDSGQSWEMISGYLYQLLAAAIKGNHTNCAQ	540
Db	481	EGILNLNLEAIDKINVTISQGFAGLAGDSGQSWEMISGYLYQLLAAAIKGNHTNCAQ	540
Qy	541	FANSNRLNWLFSRLGSOAGSGTGMLDVHLHCVLIDSPEALNMMDDEHIKVIISLLEKHGR	600
Db	541	FANSNRLNWLFSRLGSOAGSGTGMLDVHLHCVLIDSPEALNMMDDEHIKVIISLLEKHGR	600
Qy	601	DPKVLVDLCSLCVGNVAVRSSQNNICDYLLPGKNLLQTLALVDHVSVRPNIIEVGRVEG	660
Db	601	DPKVLVDLCSLCVGNVAVRSSQNNICDYLLPGKNLLQTLALVDHVSVRPNIIEVGRVEG	660
Qy	661	SAVYRKWYFEVTMDHIEKTHHMPHLRIGWANTTGYVPYPGGBKGWNGVGDDLYSYGF	720
Db	661	SAVYRKWYFEVTMDHIEKTHHMPHLRIGWANTTGYVPYPGGBKGWNGVGDDLYSYGF	720
Qy	721	DGAYLWSGGRTPVNRTHAEPYIRKGDVITGCALDLTPVIINFNPNGVRVTGSGTNTFNLE	780
Db	721	DGAYLWSGGRTPVNRTHAEPYIRKGDVITGCALDLTPVIINFNPNGVRVTGSGTNTFNLE	780
Qy	781	GMFFPVLVSCSKLSLRCFLGGEHGRRLYAAPEGYSPLVESLLPOQIISLSEPCFFYFGNLSK	840
Db	781	GMFFPVLVSCSKLSLRCFLGGEHGRRLYAAPEGYSPLVESLLPOQIISLSEPCFFYFGNLSK	840
Qy	841	RALAGPPLVQDDTAFVPTPVDTLQITLPTTYVEQIRDKLAENIHBMWAMNKIEAGWYGDQ	900
Db	841	RALAGPPLVQDDTAFVPTPVDTLQITLPTTYVEQIRDKLAENIHBMWAMNKIEAGWYGDQ	900
Qy	901	REDLHKHPCLVPPERLPPAPBKRYDIOQLAVOTLXTIILALGYIISLDKPPAIRNVRPLNE	960
Db	901	REDLHKHPCLVPPERLPPAPBKRYDIOQLAVOTLXTIILALGYIISLDKPPAIRNVRPLNE	960
Qy	961	PFMQSNQYKPAPLDLASVTLTPKMDLVDQLAENTHNLWARERIQCGWTYGLNEDSDMHR	1020
Db	961	PFMQSNQYKPAPLDLASVTLTPKMDLVDQLAENTHNLWARERIQCGWTYGLNEDSDMHR	1020
Qy	1021	SPHLVPVPKVDDAIKKANRDTASERTVRLTYVGYMLDPPPTGEQHEALLLEASKQKQADF	1080
Db	1021	SPHLVPVPKVDDAIKKANRDTASERTVRLTYVGYMLDPPPTGEQHEALLLEASKQKQADF	1080
Qy	1081	TYRAEKNYAVSSGKWYFEFEILLTAGPMRVGAHADMAPGMMLQDENSFWAPDGYNEBKVY	1140
Db	1081	TYRAEKNYAVSSGKWYFEFEILLTAGPMRVGAHADMAPGMMLQDENSFWAPDGYNEBKVY	1140
Qy	1141	SGNTESFGKQWAGDVGVFLDLIDKTIISFSLNGELLMDALGGETTFADVOGDNFVPACT	1200
Db	1141	SGNTESFGKQWAGDVGVFLDLIDKTIISFSLNGELLMDALGGETTFADVOGDNFVPACT	1200
Qy	1201	LGVGOKARLTYGQDVNTLKYFTTCGLOGBYPPFCVNMMKRDVTHWYTKDQPIFENTDEMD	1260
Db	1201	LGVGOKARLTYGQDVNTLKYFTTCGLOGBYPPFCVNMMKRDVTHWYTKDQPIFENTDEMD	1260
Qy	1261	TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWFLRLSLPVI CHNEFIDEAEKARWVE	1320
Db	1261	TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWFLRLSLPVI CHNEFIDEAEKARWVE	1320
Qy	1321	IKDRQOILMKEAVEAQMPAHIDQIMRSQFTMNDIKGLHYEDNQEBELPSSKMKRLPSRPPR	1380

Db	1321	IKDRQOILMKEAVEAQMPAHIDQIMRSQFTMNDIKGLHYEDNQEBELPSSKMKRLPSRPPR	1380
Qy	1381	KGSMTRGVITONTNINLOPGQVNGMHRTSEAEKMAKYDLGAQGLTPDDKKDKRGRSPKFF	1440
Db	1381	KGSMTRGVITONTNINLOPGQVNGMHRTSEAEKMAKYDLGAQGLTPDDKKDKRGRSPKFF	1440
Qy	1441	RSKRGSSSDRAKSRKSKTDPFSDTETVSPERGARRPNPQIKVSOAMORYNGMARPERTN	1500
Db	1441	RSKRGSSSDRAKSRKSKTDPFSDTETVSPERGARRPNPQIKVSOAMORYNGMARPERTN	1500
Qy	1501	LYGSOVGLNMATPQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEFYGVRIYPGQD	1560
Db	1501	LYGSOVGLNMATPQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEFYGVRIYPGQD	1560
Qy	1561	PTHVYIGWVTTQVHLHSKDFNQSVTKSSVIIITDDVDRVVENVNRQSCYVRADELNEY	1620
Db	1561	PTHVYIGWVTTQVHLHSKDFNQSVTKSSVIIITDDVDRVVENVNRQSCYVRADELNEY	1620
Qy	1621	MAEATAGASQGMFICGSVDSTSGSVFTCEGKDTSFKFMPEPETKLPFPAIFVEATSKEI	1680
Db	1621	MAEATAGASQGMFICGSVDSTSGSVFTCEGKDTSFKFMPEPETKLPFPAIFVEATSKEI	1680
Qy	1681	LQIELGRSATSPLSAAVLPTSQKHVIPOPPRLKVQCLKPHQWARVPNQSLQVHALKLS	1740
Db	1681	LQIELGRSATSPLSAAVLPTSQKHVIPOPPRLKVQCLKPHQWARVPNQSLQVHALKLS	1740
Qy	1741	DIRGSMWLCBDVSMALHIIPEEDRCIDILEPIEMDKLLSFHSHHTLTLYAALCQSNYRA	1800
Db	1741	DIRGSMWLCBDVSMALHIIPEEDRCIDILEPIEMDKLLSFHSHHTLTLYAALCQSNYRA	1800
Qy	1801	AHALCTHVDOKQLLYAIQSOYMSGPLRQGFYDILLIALHLESHATTMEACNKFVILPGPE	1860
Db	1801	AHALCTHVDOKQLLYAIQSOYMSGPLRQGFYDILLIALHLESHATTMEACNKFVILPGPE	1860
Qy	1861	LKALYBEPDMGHSLRSLQTESVRPQKMTDIAESIENSLYSPYFPFLEVAREFVMQALA	1920
Db	1861	LKALYBEPDMGHSLRSLQTESVRPQKMTDIAESIENSLYSPYFPFLEVAREFVMQALA	1920
Qy	1921	EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMREDVEKLLIMTNPETWDSFD	1980
Db	1921	EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMREDVEKLLIMTNPETWDSFD	1980
Qy	1981	KEGDKHRKGLLHKMAEGAKLQMCVYLQHLNDIQLRHRVEAIIAPAHDPVGLDLOTQLR	2040
Db	1981	KEGDKHRKGLLHKMAEGAKLQMCVYLQHLNDIQLRHRVEAIIAPAHDPVGLDLOTQLR	2040
Qy	2041	RYTEIKQSDDLPSAAAKTREFRCPPREQMNAILSFKHLSEEDKENCPCGEELIARMNEF	2100
Db	2041	RYTEIKQSDDLPSAAAKTREFRCPPREQMNAILSFKHLSEEDKENCPCGEELIARMNEF	2100
Qy	2101	HDTLMAHVSJLHALQEPDAAENQEPKAPGAFGLYNIINTVKELEBEAKAIEBPPKKTPE	2160
Db	2101	HDTLMAHVSJLHALQEPDAAENQEPKAPGAFGLYNIINTVKELEBEAKAIEBPPKKTPE	2160
Qy	2161	EKERKVLITOTIVNABESQIETPKLVREMFSLVROVDVAGELIRALEKTYVINAKTKLD	2220
Db	2161	EKERKVLITOTIVNABESQIETPKLVREMFSLVROVDVAGELIRALEKTYVINAKTKLD	2220
Qy	2221	VASMWVGLSQRALLPVQMSQBEELMRKELMKNVNNHTFFQHPDLIRLVRHENVNMAVM	2280
Db	2221	VASMWVGLSQRALLPVQMSQBEELMRKELMKNVNNHTFFQHPDLIRLVRHENVNMAVM	2280
Qy	2281	MNTLGRRAQQAQSDAQSSQVABDSKEKOTSHEMVWVACCRFLCYFCBTGRQONKAMPDHF	2340
Db	2281	MNTLGRRAQQAQSDAQSSQVABDSKEKOTSHEMVWVACCRFLCYFCBTGRQONKAMPDHF	2340
Qy	2341	DFLLENSNILLSPSLRGSTPLDVAYSSLMNTLALALREHYLEKIAVYLSRCGLQSN	2400
Db	2341	DFLLENSNILLSPSLRGSTPLDVAYSSLMNTLALALREHYLEKIAVYLSRCGLQSN	2400
Qy	2401	ELVEKGYPDLGWDPVBERGYLDFRCVWVNGESVEENANLVIRLLLRRECEJGALURGE	2460



Db 2401 ELVEXGYFDLGMWDPVEGBERYDLRFVWNGESVEENANLVIRLLIRRPCGLGALRGE 2460  
Qy 2461 GEGLLKAIIVDANKMSERADRRKLREMOEGDVNFSPHLPESDEDEDYIDTGAALNFYC 2520  
Db 2461 GEGLLKAIIVDANKMSERADRRKLREMOEGDVNFSPHLPESDEDEDYIDTGAALNFYC 2520  
Qy 2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFPLNPPAAGEERP 2580  
Db 2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFPLNPPAAGEERP 2580  
Qy 2581 SDMPGSLIPGHKQSVGLFLERYGTEGTELFXKLLLEAFPLDPLRAATMLDRNDGCESDMA 2640  
Db 2581 SDMPGSLIPGHKQSVGLFLERYGTEGTELFXKLLLEAFPLDPLRAATMLDRNDGCESDMA 2640  
Qy 2641 LSNRYIGNSILPLLIKHAYFNEAENVASLLDATHVTYRLSKVRMLTKGOREAVSDFL 2700  
Db 2641 LSNRYIGNSILPLLIKHAYFNEAENVASLLDATHVTYRLSKVRMLTKGOREAVSDFL 2700  
Qy 2701 VALTSAMQPSMLLKLRLKLTVDVSKLSBYTTVALRLLTLHYERCAKYTGSTGAGGAFGA 2760  
Db 2701 VALTSAMQPSMLLKLRLKLTVDVSKLSBYTTVALRLLTLHYERCAKYTGSTGAGGAFGA 2760  
Qy 2761 SSDEBKRLTMMLFNSIFOSLSKMDYEPBLFGKALPCLIAIGCALPPDYSLSKNYDDEFG 2820  
Db 2761 SSDEBKRLTMMLFNSIFOSLSKMDYEPBLFGKALPCLIAIGCALPPDYSLSKNYDDEFG 2820  
Qy 2821 KEQAAGDLDNPOYPQIPNTSSVALNNDLNTTVOKFSESHYHDAMASRKIENGWYGEQWS 2880  
Db 2821 KEQAAGDLDNPOYPQIPNTSSVALNNDLNTTVOKFSESHYHDAMASRKIENGWYGEQWS 2880  
Qy 2881 DSQKTHPRLPKNMNLNDYKERYKEPVRESIKALLAIGWSVEHSEVDI PSNNRSMRRQS 2940  
Db 2881 DSQKTHPRLPKNMNLNDYKERYKEPVRESIKALLAIGWSVEHSEVDI PSNNRSMRRQS 2940  
Qy 2941 KSGRPPBEIVTDSATPFDPNHPVDMTNLTLSREMNMAERLADNAHDIWAKKKKEELVT 3000  
Db 2941 KSGRPPBEIVTDSATPFDPNHPVDMTNLTLSREMNMAERLADNAHDIWAKKKKEELVT 3000  
Qy 3001 NGGGTHPOLVPYDLITDKEKKORRSQEFKLYQYQYKLRHPSKAPQSDTEQTTTGA 3060  
Db 3001 NGGGTHPOLVPYDLITDKEKKORRSQEFKLYQYQYKLRHPSKAPQSDTEQTTTGA 3060  
Qy 3061 TELRPAYSILLEKLIQYIDRATINMKLLKPSFTFSRRSFKTSTRDJKFPSKAVLPLMEKY 3120  
Db 3061 TELRPAYSILLEKLIQYIDRATINMKLLKPSFTFSRRSFKTSTRDJKFPSKAVLPLMEKY 3120  
Qy 3121 FSTHRYNFIATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAGPDVRIITVRCLQV 3180  
Db 3121 FSTHRYNFIATATNNVGAASLKEKEMVAALFCKLASLLRSRLAAGPDVRIITVRCLQV 3180  
Qy 3181 LVKGIIDAKSLVKNCPDEFIRTSMLTFPNVADDVGHITIMNLQDKYAHLRGTHLKTSTSLG 3240  
Db 3181 LVKGIIDAKSLVKNCPDEFIRTSMLTFPNVADDVGHITIMNLQDKYAHLRGTHLKTSTSLG 3240  
Qy 3241 YINGVLLPLLTAKFPHLANCCEYGDILLDEIOVASVKMGSUYALGTASLTHDRKYLKT 3300  
Db 3241 YINGVLLPLLTAKFPHLANCCEYGDILLDEIOVASVKMGSUYALGTASLTHDRKYLKT 3300  
Qy 3301 EIERHKPALGSCLGAFSSFTFPVAFLEPHLNKINQFSLNRIADHSLEAQDIMQKMEQCMP 3360  
Db 3301 EIERHKPALGSCLGAFSSFTFPVAFLEPHLNKINQFSLNRIADHSLEAQDIMQKMEQCMP 3360  
Qy 3361 TLETILGEVDQFVESDKTYNEAPHIIDVVLPPLCSYLPFWMAQQPDNVTPTGNGHVTMT 3420  
Db 3361 TLETILGEVDQFVESDKTYNEAPHIIDVVLPPLCSYLPFWMAQQPDNVTPTGNGHVTMT 3420  
Qy 3421 AEHMQNQLKNVLKLIKKNIGNENAPMTFIATYTOQIINSSEELLRDSFLPLAERVRKR 3480  
Db 3421 AEHMQNQLKNVLKLIKKNIGNENAPMTFIATYTOQIINSSEELLRDSFLPLAERVRKR 3480  
Qy 3481 TDNMFHKEESLRGFTIKSSTDDTSQVESIQEWDQLLVRIYISFYPLLKIKYVDLQRNHWLR 3540  
Db 3481 TDNMFHKEESLRGFTIKSSTDDTSQVESIQEWDQLLVRIYISFYPLLKIKYVDLQRNHWLR 3540

Qy 3541 NNVEPEBELYNHVAEIIFNIMWSKQYFLKBEQNFISANEIDNMVLIMPTATRRVTAVTGDT 3600  
Db 3541 NNVEPEBELYNHVAEIIFNIMWSKQYFLKBEQNFISANEIDNMVLIMPTATRRVTAVTGDT 3600  
Qy 3601 PQGGKKKKKRDVKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQLVHCKDRFLKK 3660  
Db 3601 PQGGKKKKKRDVKRDKDKEVQASLMVACLKRLLPVGLNLFAGREQLVHCKDRFLKK 3660  
Qy 3661 MSEODVAEFAKTQTLTLPDKIDPADEMSWOHLVSKLSKSKSNITVETAEKAKIIDDV 3720  
Db 3661 MSEODVAEFAKTQTLTLPDKIDPADEMSWOHLVSKLSKSKSNITVETAEKAKIIDDV 3720  
Qy 3721 ERIVAMSKVLFGHMDHPQOMSKNVYRSVSIQRKRAVIACFRQTSLSHSLPRHRACNIF 3780  
Db 3721 ERIVAMSKVLFGHMDHPQOMSKNVYRSVSIQRKRAVIACFRQTSLSHSLPRHRACNIF 3780  
Qy 3781 ARTTYELWLEBENIGOEVMIEDLTQSFEDABELKSDVVVEGEKDPDLTQLVTTFCRGAMT 3840  
Db 3781 ARTTYELWLEBENIGOEVMIEDLTQSFEDABELKSDVVVEGEKDPDLTQLVTTFCRGAMT 3840  
Qy 3841 ERSALQEDPLMYSVAHIIAKSCGEEBEGGEBEGGEGGAEABDEGRASITHEQEMEKOK 3900  
Db 3841 ERSALQEDPLMYSVAHIIAKSCGEEBEGGEBEGGEGGAEABDEGRASITHEQEMEKOK 3900  
Qy 3901 LLFHOARLADRGVAEMVLLHISASGKLPSSEVMVMTLQLGISILRGGNIDIQMGMLNHLKD 3960  
Db 3901 LLFHOARLADRGVAEMVLLHISASGKLPSSEVMVMTLQLGISILRGGNIDIQMGMLNHLKD 3960  
Qy 3961 KCDVGFPTSIAGLMNSCSVLDDAFERNTKAEGLVGLEGAABGKNMHDAFTCALPRFI 4020  
Db 3961 KCDVGFPTSIAGLMNSCSVLDDAFERNTKAEGLVGLEGAABGKNMHDAFTCALPRFI 4020  
Qy 4021 QLTCEGHNLDQNYLRTQAGNTTNNVICTVDVYLRLQESIMDFYHYSKELIDPAGK 4080  
Db 4021 QLTCEGHNLDQNYLRTQAGNTTNNVICTVDVYLRLQESIMDFYHYSKELIDPAGK 4080  
Qy 4081 ANFFKALGVASQVFNLTTEVIQGPCTONQOALAHSLRWDVAGGFLFLFSHMQDKLSKSHS 4140  
Db 4081 ANFFKALGVASQVFNLTTEVIQGPCTONQOALAHSLRWDVAGGFLFLFSHMQDKLSKSHS 4140  
Qy 4141 QVDLLKELLNLQKDMI PMMLSMLEGNVNGTIGQMVDTLVESASNVBELILKYFOMFLKL 4200  
Db 4141 QVDLLKELLNLQKDMI PMMLSMLEGNVNGTIGQMVDTLVESASNVBELILKYFOMFLKL 4200  
Qy 4201 KDLTSSASFQIBDANNQDGVLPKDFKEXMEQOKSYTPEEIEFLLACCETNHDGKLDYIGF 4260  
Db 4201 KDLTSSASFQIBDANNQDGVLPKDFKEXMEQOKSYTPEEIEFLLACCETNHDGKLDYIGF 4260  
Qy 4261 CDRFHEPAKEIGFNLAVLLTNLSHEMPNEPRLARFLETAGSVLNYFEFPLGRIEIMGSK 4320  
Db 4261 CDRFHEPAKEIGFNLAVLLTNLSHEMPNEPRLARFLETAGSVLNYFEFPLGRIEIMGSK 4320  
Qy 4321 RIERVYFEIKESNIEQMEKPOIKESKRAFFYSIVTEGGDKKELEAFVNFCEDAIPEMTHA 4380  
Db 4321 RIERVYFEIKESNIEQMEKPOIKESKRAFFYSIVTEGGDKKELEAFVNFCEDAIPEMTHA 4380  
Qy 4381 SGLMAAESVESVGGTKNREASWYMGDDDDERAGKDPFRGLOSVKDGATAFSSLSPSNI 4440  
Db 4381 SGLMAAESVESVGGTKNREASWYMGDDDDERAGKDPFRGLOSVKDGATAFSSLSPSNI 4440  
Qy 4441 KAKTADMOQMPAPAEFLAVGFFKMFVLYLGVGLVVRVYIFGVLLGLMRGPQTDPEPPE 4500  
Db 4441 KAKTADMOQMPAPAEFLAVGFFKMFVLYLGVGLVVRVYIFGVLLGLMRGPQTDPEPPE 4500  
Qy 4501 PTEBEKIQOLRHRLLIATOSSRHLPALPPADDTGQMVSAFGLDITTKEDNGOIQVKPHESP 4560  
Db 4501 PTEBEKIQOLRHRLLIATOSSRHLPALPPADDTGQMVSAFGLDITTKEDNGOIQVKPHESP 4560  
Qy 4561 STSTPSSGEEAEVSPDESADHTEBQRPPSLIDLGGEOAKKQOABERMAQAAQAAAMGAI 4620  
Db 4561 STSTPSSGEEAEVSPDESADHTEBQRPPSLIDLGGEOAKKQOABERMAQAAQAAAMGAI 4620





1141 QY SGNTEFGKOWAGDVGVFLDLIDKTTISFSLNGELLMDALGGTTTADVOGDNFVPACT 1200  
1141 DB SGNTEFGKOWAGDVGVFLDLIDKTTISFSLNGELLMDALGGTTTADVOGDNFVPACT 1200  
1201 QY LGVGQKARLTGYQDVNTLYKYFTTCGLQBGYPFCVNMKRDYTHWYTKDQPIFENTDEMID 1260  
1201 DB LGVGQKARLTGYQDVNTLYKYFTTCGLQBGYPFCVNMKRDYTHWYTKDQPIFENTDEMID 1260  
1261 QY TRIDVTRIPAGSDTPPCLKI SHNTFETMEKANWFLRLSLPVI CHNEFIDEAEKARWVE 1320  
1261 DB TRIDVTRIPAGSDTPPCLKI SHNTFETMEKANWFLRLSLPVI CHNEFIDEAEKARWVE 1320  
1321 QY IKDRQOILMKAEVAQMPAHIDQIMRSGFTWMDIKGLHYEDNQBELPSSKMRLPSRPPR 1380  
1321 DB IKDRQOILMKAEVAQMPAHIDQIMRSGFTWMDIKGLHYEDNQBELPSSKMRLPSRPPR 1380  
1381 QY KGSMTRGVTIQNYNNLQPGVNGMHRSTSEAEAKYDLGAQGLTPDDKDKRGRSPPKFF 1440  
1381 DB KGSMTRGVTIQNYNNLQPGVNGMHRSTSEAEAKYDLGAQGLTPDDKDKRGRSPPKFF 1440  
1441 QY RSKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNPQIKVSOANQRYNGMNAARPSRTN 1500  
1441 DB RSKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNPQIKVSOANQRYNGMNAARPSRTN 1500  
1501 QY LYGSOVLNMTPTQDRKQMTTSTLQAQATETVGNEIFDAECLKLINEFYFVGRIYPOQD 1560  
1501 DB LYGSOVLNMTPTQDRKQMTTSTLQAQATETVGNEIFDAECLKLINEFYFVGRIYPOQD 1560  
1561 QY PTHYVIGWVTQYHLHSDFNQSKVTKSSVITDDYDRVVENVRNQSCYMYRABEYNEV 1620  
1561 DB PTHYVIGWVTQYHLHSDFNQSKVTKSSVITDDYDRVVENVRNQSCYMYRABEYNEV 1620  
1621 QY MAETAKGASQGMFTGCSVDSTSGVSTCSGKOTSFVKMEPETKLPPIAFVETATSKBI 1680  
1621 DB MAETAKGASQGMFTGCSVDSTSGVSTCSGKOTSFVKMEPETKLPPIAFVETATSKBI 1680  
1681 QY LOIELGRATSILPISAAVLPTSDKHVIPQFPRLKVQCLKPHQWARVFNQSLQVHALKLS 1740  
1681 DB LOIELGRATSILPISAAVLPTSDKHVIPQFPRLKVQCLKPHQWARVFNQSLQVHALKLS 1740  
1741 QY DIRGSMCEDAVSMALHPIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800  
1741 DB DIRGSMCEDAVSMALHPIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800  
1801 QY AHALCTHVQDKQLYAIQSYMSGPLRQGFYDILLIALHLESHATTMEACKNEFVPLGPE 1860  
1801 DB AHALCTHVQDKQLYAIQSYMSGPLRQGFYDILLIALHLESHATTMEACKNEFVPLGPE 1860  
1861 QY LKALYEEPDGMGHSLSLQTESVVRPOMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920  
1861 DB LKALYEEPDGMGHSLSLQTESVVRPOMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920  
1921 QY EAVETNOVHNRDPVGGSNENILPLILKLVDRLLLVMGMRDEDEKLLIMTNPETWDPSPD 1980  
1921 DB EAVETNOVHNRDPVGGSNENILPLILKLVDRLLLVMGMRDEDEKLLIMTNPETWDPSPD 1980  
1981 QY KEGKDEHRKGLLHMKAQSGAKLQWCYLLQHLNDIQLRHVRBAI IAFAHDFVGDLOTQDLR 2040  
1981 DB KEGKDEHRKGLLHMKAQSGAKLQWCYLLQHLNDIQLRHVRBAI IAFAHDFVGDLOTQDLR 2040  
2041 QY RYTEIKQSDLPASVAAKKTREPCPREQMNAILSPKHLBEDKENCPCGEBELIARMNEF 2100  
2041 DB RYTEIKQSDLPASVAAKKTREPCPREQMNAILSPKHLBEDKENCPCGEBELIARMNEF 2100  
2101 QY HDTLMAHVSLLHALQBPDAENQEPKAPGAFGLKLYNIINTVKLEBEEAKAIEEPPKKTPE 2160  
2101 DB HDTLMAHVSLLHALQBPDAENQEPKAPGAFGLKLYNIINTVKLEBEEAKAIEEPPKKTPE 2160  
2161 QY EKFRKVLQITI VNWAEESQIETPKLVREMFSLLVRQYDAVGLIPALEKTYVINAKTKLD 2220  
2161 DB EKFRKVLQITI VNWAEESQIETPKLVREMFSLLVRQYDAVGLIPALEKTYVINAKTKLD 2220

2221 QY VAEWMVGLSQIRALLPVQMSQEBEELMRKRLWKL VNNHTTFFQHPDLIRLVRVHNVMVAM 2280  
2221 DB VAEWMVGLSQIRALLPVQMSQEBEELMRKRLWKL VNNHTTFFQHPDLIRLVRVHNVMVAM 2280  
2281 QY MNTLGRRAQASDAQSPSQVAEDSKKDTSHEMVACCRFLCYFCFCTGRQNOKAMFDHF 2340  
2281 DB MNTLGRRAQASDAQSPSQVAEDSKKDTSHEMVACCRFLCYFCFCTGRQNOKAMFDHF 2340  
2341 QY DFLLENSNILLSPRLSGSTPLDVAYSSLMENTEALALAREHYLEKIAVLISRLCGLQSN 2400  
2341 DB DFLLENSNILLSPRLSGSTPLDVAYSSLMENTEALALAREHYLEKIAVLISRLCGLQSN 2400  
2401 QY ELVEKGYDPLGWDPEVEGERYLDLRF CVWNGESVEENANLIRLLIRRPCLGPAURGE 2460  
2401 DB ELVEKGYDPLGWDPEVEGERYLDLRF CVWNGESVEENANLIRLLIRRPCLGPAURGE 2460  
2461 QY GEGLLKAI VDKANKMSERIA DRKRLREMEQGDVNFSPHLPESDEDEYIDTGAAILNFCY 2520  
2461 DB GEGLLKAI VDKANKMSERIA DRKRLREMEQGDVNFSPHLPESDEDEYIDTGAAILNFCY 2520  
2521 QY TLVDLLGRCAPDAGVIALGKNESLRARAILRSILVPLEDLQGLSLRFTLNNPAAAGEERP 2580  
2521 DB TLVDLLGRCAPDAGVIALGKNESLRARAILRSILVPLEDLQGLSLRFTLNNPAAAGEERP 2580  
2581 QY SDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEBAFLPDLRAATMLDRNDGCESDMA 2640  
2581 DB SDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLEBAFLPDLRAATMLDRNDGCESDMA 2640  
2641 QY LSMNRYTGNISILPLLIKHAYFYNEAENYASLLDATHVTYVRLSKVRMLTKQOREAVSDFL 2700  
2641 DB LSMNRYTGNISILPLLIKHAYFYNEAENYASLLDATHVTYVRLSKVRMLTKQOREAVSDFL 2700  
2701 QY VALTSAMQPSMMLKLRKLTVDVSKLSEYTTVALRLTLHYERC AKYVYSTGAGQAFGA 2760  
2701 DB VALTSAMQPSMMLKLRKLTVDVSKLSEYTTVALRLTLHYERC AKYVYSTGAGQAFGA 2760  
2761 QY SSDEEKLTMWLFNSNIFDLSLKM DYEPFLFGKALPCLIAIGCALPPDYSLSKNYDDPEYG 2820  
2761 DB SSDEEKLTMWLFNSNIFDLSLKM DYEPFLFGKALPCLIAIGCALPPDYSLSKNYDDPEYG 2820  
2821 QY KEQAAGOLDNPQYDPOPI NTSSVALNNDLNTIVQKFSEHYHDASRKRIENGWYGEWS 2880  
2821 DB KEQAAGOLDNPQYDPOPI NTSSVALNNDLNTIVQKFSEHYHDASRKRIENGWYGEWS 2880  
2881 QY DSQKTHPRKLPYNNMLNDYEKERYKEPVRESIKALLAIGWSVEHSEVDIPSNRRSMRRQS 2940  
2881 DB DSQKTHPRKLPYNNMLNDYEKERYKEPVRESIKALLAIGWSVEHSEVDIPSNRRSMRRQS 2940  
2941 QY KSGGRPPEIV-TDSATPFDYNNPVPDVTNLTLSREM QNMAERLADNAHDIWAKKKCEBLV 2999  
2941 DB KSGGRPPEIV-TDSATPFDYNNPVPDVTNLTLSREM QNMAERLADNAHDIWAKKKCEBLV 3000  
3000 QY TNGGGIHPQLVPYDILLTDKEKKDORERSQBELKYLOYGKYLHRPSKAPQSDTQTTTGV 3059  
3001 DB TNGGGIHPQLVPYDILLTDKEKKDORERSQBELKYLOYGKYLHRPSKAPQSDTQTTTGV 3060  
3060 QY AIELREAYSLLEKLIQYIDRATINMKLLKPBSTTFSSRSSPKTSTRD IKFFSKAVLPLMEK 3119  
3061 DB AIELREAYSLLEKLIQYIDRATINMKLLKPBSTTFSSRSSPKTSTRD IKFFSKAVLPLMEK 3120  
3120 QY YFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLRLSRALAAPGDPVIRVCLQ 3179  
3121 DB YFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLRLSRALAAPGDPVIRVCLQ 3180  
3180 QY VLVKGIDAKSLVKQCPBFIRTSMLTFFNNVADDVGHITIMNLDGKYAHLRGTHLKTSTSL 3239  
3181 DB VLVKGIDAKSLVKQCPBFIRTSMLTFFNNVADDVGHITIMNLDGKYAHLRGTHLKTSTSL 3240  
3240 QY GYINGVLLPILTAKFDHLANCEYCADILLDEIQVASYKMLGSLVALGTASITDHRKYLK 3299  
3241 DB GYINGVLLPILTAKFDHLANCEYCADILLDEIQVASYKMLGSLVALGTASITDHRKYLK 3300  
3300 QY TEIERHKPALGSCGLGAFSSTFPVAFLEPHLKNRQFSLNRIADHSLEA QDIMQMEQCM 3359

Db 3301 TEIERHPALGSCJGAFSSTFPVAFLEPHLNKHQFSLNRIADHSLEAQDIMQMEQCM 3360  
Qy 3360 PTLETIGEVDQFVESDKTYNEAPHIIDVVLPLICSVLPFWMAQPDNVPTGNGHVTMV 3419  
Db 3361 PTLEAILGEVDQFVESDKTYNEAPHIIDVVLPLICSVLPFWMAQPDNVPTGNGHVTMV 3420  
Qy 3420 TAEHNNQLKNVLKLIKIGNENAPWMTTRTATVTOQIIINSSEELRDSFLPLAERVK 3479  
Db 3421 TAEHNNQLKNVLKLIKIGNENAPWMTTRTATVTOQIIINSSEELRDSFLPLAERVK 3480  
Qy 3480 RTDNMFKEESLRGFIKSDTDDTSQVESQIQEDQOLLVRDIYSFYPLLIIKYVDLQRNHWL 3539  
Db 3481 RTDNMFKEESLRGFIKSDTDDTSQVESQIQEDQOLLVRDIYSFYPLLIIKYVDLQRNHWL 3540  
Qy 3540 RNNVPEABELYNHVAEIPNIWSKYQFLKEQNFISANEIDNMVLIIMPTATRRVTAATDG 3599  
Db 3541 RNNVPEABELYNHVAEIPNIWSKYQFLKEQNFISANEIDNMVLIIMPTATRRVTAATDG 3600  
Qy 3600 TPQGGGKKKKHRDKRDKDKEVOASLMVACLKELLPVGLNLFAGRQELVQHCKDRFP-- 3657  
Db 3601 TPQGGGKKKKHRDKRDKDKEVOASLMVACLKELLPVGLNLFAGRQELVQHCKDRFLK 3660  
Qy 3658 ---LKKMSEQDVAEFAKTQLTLDPKIDPADMSWQHLYLSKLGSKSNITVETAENKAK 3714  
Db 3661 VGTLLKKSEQDVAEFAKTQLTLDPKIDPADMSWQHLYLSKLGSKSNITVETAENKAK 3720  
Qy 3715 IIDTVERIVAMSKVLFGLMHIDHPQQMSKNVRSVVSIOKRAVIACFRQTSLSHSLPRH 3774  
Db 3721 IIDTVERIVAMSKVLFGLMHIDHPQQMSKNVRSVVSIOKRAVIACFRQTSLSHSLPRH 3780  
Qy 3775 RACNIFARTYVELLEENIQOEVMIEDLTOSFEDAELKSDVVEGEKDPDLTQLVTTF 3834  
Db 3781 RACNIFARTYVELLEENIQOEVMIEDLTOSFEDAELKSDVVEGEKDPDLTQLVTTF 3840  
Qy 3835 CRGAMTERSGALQBDPLVMSYAHIIAKSCGEEEBEGGEEBEGGEEBAEDEGRASITHEQ 3894  
Db 3841 CRGAMTERSGALQBDPLVMSYAHIIAKSCGEEEBEGGEEBEGGEEBAEDEGRASITHEQ 3900  
Qy 3895 EMEQKQLFHQARLADRGVAEMVLLHISAKGLSPSEVMWMTLQGISILRGNDIDIQMG 3954  
Db 3901 EMEQKQLFHQARLADRGVAEMVLLHISAKGLSPSEVMWMTLQGISILRGNDIDIQMG 3960  
Qy 3955 LNHLKDKDVGFFTSIAGLNMNSCVLDLDAFERNTKAEGLGVLEGAAGEKNMHDAEFTC 4014  
Db 3961 LNHLKDKDVGFFTSIAGLNMNSCVLDLDAFERNTKAEGLGVLEGAAGEKNMHDAEFTC 4020  
Qy 4015 ALPRFIQJLTCEGHNLDWQNYLRTQAGNTTIVNVVICTVDYLLRLQESIMDFYWHYSKEL 4074  
Db 4021 ALPRFIQJLTCEGHNLDWQNYLRTQAGNTTIVNVVICTVDYLLRLQESIMDFYWHYSKEL 4080  
Qy 4075 IDPAGKANFFKAIGVASQVFNLTLEVIQGPCTQOQALAHSLRLWDAVGGFLFLFSHQDK 4134  
Db 4081 IDPAGKANFFKAIGVASQVFNLTLEVIQGPCTQOQALAHSLRLWDAVGGFLFLFSHQDK 4140  
Qy 4135 LSKUSSQVLLKELLNLQKDMIPMLSMLEGNVNGTIGQMWDTLVESASNVELLILKYF 4194  
Db 4141 LSKUSSQVLLKELLNLQKDMITWMLSMLEGNVNGTIGQMWDTLVESASNVELLILKYF 4200  
Qy 4195 DMFLKLDLTSSASFOEIDANNQDWLPKDPKEKMEQKSYTPPEIEBFLACCTNHDGK 4254  
Db 4201 DMFLKLDLTSSASFOEIDANNQDWLPKDPKEKMEQKSYTPPEIEBFLACCTNHDGK 4260  
Qy 4255 LDYIGFCDRFPEAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIE 4314  
Db 4261 LDYIGFCDRFPEAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNYFEPFLGRIE 4320  
Qy 4315 IMGSKRIERYVFEIKESNIQWEKPKQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAI 4374  
Db 4321 IMGSKRIERYVFEIKESNIQWEKPKQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAI 4380  
Qy 4375 FEMTHASGLMAASESVGGTKNREASVYMGDDDDDERAGKDPFRRLGLQSKVDGVATAFSS 4434

Db 4381 FEMTHASGLMAASESVGGTKNREASVYMGDDDDDERAGKDPFRRLGLQSKVDGVATAFSS 4440  
Qy 4435 LSPSNIKAKIADNQOQPPAELAVGFFKMPFYLFFVLYGCVGLVVVRYIFGLVLLGLMRGPQT 4494  
Db 4441 LSPSNIKAKIADNQOQPPAELAVGFFKMPFYLFFVLYGCVGLVVVRYIFGLVLLGLMRGPQT 4500  
Qy 4495 DEPPPTPEEKEIGQLRHRLLATQSSRHLPALPADDTGOMQVSAGFLDITTKEDNGQIQV 4554  
Db 4501 DEPPPTPEEKEIGQLRHRLLATQSSRHLPALPADDTGOMQVSAGFLDITTKEDNGQIQV 4560  
Qy 4555 KPHEPSTSTPSSGEEAEVSPDESADHTEBQRPSPSLIDLGGQKQAKQAEERMAQAAQ 4614  
Db 4561 KPHEPSTSTPSSGEEAEVSPDESADHTEBQRPSPSLIDLGGQKQAKQAEERMAQAAQ 4620  
Qy 4615 AANSAIEASKXAVQGPAPALSQVDLSQYTRAVSFLENFYNLKVVALVLAFCINFVL 4674  
Db 4621 AANSAIEASKXAVQGPAPALSQVDLSQYTRAVSFLENFYNLKVVALVLAFCINFVL 4680  
Qy 4675 LFYKVSITLDGEGGEGGLGDIAGGGSGGAGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 4734  
Db 4681 LFYKVSITLDGEGGEGGLGDIAGGGSGGAGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 4740  
Qy 4735 MEHVIKMAAVLHSISVSLAILIGYHYHLKVPLAIFKREKEIARKLEFFDGLYIAEQPEDDDLK 4794  
Db 4741 MEHVIKMAAVLHSISVSLAILIGYHYHLKVPLAIFKREKEIARKLEFFDGLYIAEQPEDDDLK 4800  
Qy 4795 SHWDLKVISAKSPVNVWDKFKVKKYRAKYSETYDFDSISNMLGMEKTSFSAQEEGSKG 4854  
Db 4801 SHWDLKVISAKSPVNVWDKFKVKKYRAKYSETYDFDSISNMLGMEKTSFSAQEEGSKG 4860  
Qy 4855 LIHYIINIDRWYQWKAQVTTITDNSFLYLSLWYFSFVSMGNFNNFFFAAHLILDVAVGPKTL 4914  
Db 4861 LIHYIINIDRWYQWKAQVTTITDNSFLYLSLWYFSFVSMGNFNNFFFAAHLILDVAVGPKTL 4920  
Qy 4915 RTILQSVTHNGKQVLVTMLLTIIVYITVIAFNFRKRYVQBEDDEVNRNCHDMLTCFV 4974  
Db 4921 RTILQSVTHNGKQVLVTMLLTIIVYITVIAFNFRKRYVQBEDDEVNRNCHDMLTCFV 4980  
Qy 4975 FNLKYGVRAGGGTGDELEPPDGDSEVYRIIFDISFFFIIVILLALQGLIIDAFCGLR 5034  
Db 4981 FNLKYGVRAGGGTGDELEPPDGDSEVYRIIFDISFFFIIVILLALQGLIIDAFCGLR 5040  
Qy 5035 DQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTTEY 5094  
Db 5041 DQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANYMFFLMHLINKPDTTEY 5100  
Qy 5095 GQSTYVNMNYTORCWDFFPVGDCFRKQYEDLMGE 5128  
Db 5101 GQSTYVNMNYTORCWDFFPVGDCFRKQYEDLMGE 5134

## RESULT 3

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Db 1981 PETWPSFDKGGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2040  
Qy 2032 GDLOTDLRRYTEIKQSDLPASVAAKKTRPRCPRPROMNAILSFKHLEEDKENCPCGE 2091  
Db 2041 GDLOTDLRRYTEIKQSDLPASVAAKKTRPRCPRPROMNAILSFKHLEEDKENCPCGE 2100  
Qy 2092 ELIARMNEFHDTLMAHVSLSHALQSPDAENOEPAKPGAFGKLYNIINTVKELEEEAKAI 2151  
Db 2101 ELIARMNEFHDTLMAHVSLSHALQSPDAENOEPAKPGAFGKLYNIINTVKELEEEAKAI 2160  
Qy 2152 EEPKPKTPEEKFRKVIQTIIVNMAEESQIETPKLVREMFSLLRQYDAVGELIRALEKTY 2211  
Db 2161 EEPKPKTPEEKFRKVIQTIIVNMAEESQIETPKLVREMFSLLRQYDAVGELIRALEKTY 2220  
Qy 2212 VINAKTKLDVAMVMVGLSQIRALLPVQMSQBEELMRKRLWKLVNNHTFFQHPDLIRVL 2271  
Db 2221 VINAKTKLDVAMVMVGLSQIRALLPVQMSQBEELMRKRLWKLVNNHTFFQHPDLIRVL 2280  
Qy 2272 VHENVMAVMNNTLGRRAQAQSDAPSSQOPVAEDSKEDTSHVMVACCRFLCYFCRTGRQ 2331  
Db 2281 VHENVMAVMNNTLGRRAQAQSDAPSSQOPVAEDSKEDTSHVMVACCRFLCYFCRTGRQ 2340  
Qy 2332 NOKAMFHFDFLENSNILLRSPSLRGSTPLDVAYSLSMENTELALREHYLEKIAVYL 2391  
Db 2341 NOKAMFHFDFLENSNILLRSPSLRGSTPLDVAYSLSMENTELALREHYLEKIAVYL 2400  
Qy 2392 SRCGLQNSSELVEKGYPDGLGWDPEGERYLDFLFCFVWVNGESVEENANLIRLLIRPE 2451  
Db 2401 SRCGLQNSSELVEKGYPDGLGWDPEGERYLDFLFCFVWVNGESVEENANLIRLLIRPE 2460  
Qy 2452 CLGPAALRGEGLLKAIVDANKMSERTADRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511  
Db 2461 CLGPAALRGEGLLKAIVDANKMSERTADRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520  
Qy 2512 GAAILNFYCTLVLDLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571  
Db 2521 GAAILNFYCTLVLDLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580  
Qy 2572 PAAGEERPKDMPSGLLPGHKQSGVGLFLERVYGIETQELFYKLEEAFLPDLRAATMLDR 2631  
Db 2581 PAAGEERPKDMPSGLLPGHKQSGVGLFLERVYGIETQELFYKLEEAFLPDLRAATMLDR 2640  
Qy 2632 NDCESDWMALSMNRYIGNSILPLIKHAYFYNEAENYASLLDATLHTVYRLSKRMMLTKG 2691  
Db 2641 NDCESDWMALSMNRYIGNSILPLIKHAYFYNEAENYASLLDATLHTVYRLSKRMMLTKG 2700  
Qy 2692 QREAVSDPLVALTSAMQPSMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751  
Db 2701 QREAVSDPLVALTSAMQPSMLLKLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760  
Qy 2752 GAGQAGFAGSDEEKRLTMMLFSNIFDLSLKWDEYEPFLFGKALPCLIAIGCALPPDYSL 2811  
Db 2761 GAGQAGFAGSDEEKRLTMMLFSNIFDLSLKWDEYEPFLFGKALPCLIAIGCALPPDYSL 2820  
Qy 2812 KNYDDFVYKQCAAGDLNDPQDPQINTSSVALNNDLNTTVQFSEHYHDAMASRKIEN 2871  
Db 2821 KNYDGEFYKQCAAGDLNDPQDPQINTSSVALNNDLNTTVQFSEHYHDAMASRKIEN 2880  
Qy 2872 GWVYGEHSDSQKTHPRLLKPNMNLNDYKERYKEPVRESLKALLAIGWSVEHSVDIPSN 2931  
Db 2881 GWVYGEHSDSQKTHPRLLKPNMNLNDYKERYKEPVRESLKALLAIGWSVEHSVDIPSN 2940  
Qy 2932 NRSSMRQSGSGGRPPEIVTDSATPFDPYNPHVDMTNLTLRSREMNMAERLADNAHDIA 2991  
Db 2941 NRSSMRQSGSGGRPPEIVTDSATPFDPYNPHVDMTNLTLRSREMNMAERLADNAHDIA 3000  
Qy 2992 KKKKEELVTNNGGTHPQLVPYDILLTDKSKKDRERSQEBFLKYLOYQGYKLHRPSKAPQSD 3051  
Db 3001 KKKKEELVTNNGGTHPQLVPYDILLTDKSKKDRERSQEBFLKYLOYQGYKLHRPSKAPQSD 3060  
Qy 3052 TEQTTTGVAIELRFPAYSILLEKLIQYIDRATINMKLLKPSTTFSRRSFKTSTRDIKFPFSK 3111  
Db 3061 TEQTTTGVAIELRFPAYSILLEKLIQYIDRATINMKLLKPSTTFSRRSFKTSTRDIKFPFSK 3120

Qy 3112 AVLPLMEKYPSTHRNYFIAVATATNNVGAASLAKEMVAALFCKLASLLRSRLAAFGPDV 3171  
Db 3121 VVLPLMEKYPSTHRNYFIAVATATNNVGAASLAKEMVAALFCKLASLLRSRLAAFGPDV 3180  
Qy 3172 RIIVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQDGKYAHLRGT 3231  
Db 3181 RIIVRCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITMNLQDGKYAHLRGT 3240  
Qy 3232 HLKTSLSGVINGVILLPILTAKEPDHLANCEYAGADLLDEIQVASYKMLGSLYALGTDA 3291  
Db 3241 HLKTSLSGVINGVILLPILTAKEPDHLANCEYAGADLLDEIQVASYKMLGSLYALGTDA 3300  
Qy 3292 THDRKYLKTEIERHKALGSCIGAFSTFPVAFLEPHLNKNQFSLNLRNADHSLEAQDI 3351  
Db 3301 THDRKYLKTEIERHKALGSCIGAFSTFPVAFLEPHLNKNQFSLNLRNADHSLEAQDI 3360  
Qy 3352 MQKMEQCMPTLETILGEVQDFVESDKTYNEAPHIIDVLPPLLCYLPFFMWAQGPNDVTPT 3411  
Db 3361 MQKMEQCMPTLETILGEVQDFVESDKTYNEAPHIIDVLPPLLCYLPFFMWAQGPNDVTPT 3420  
Qy 3412 GGNHVTMTVAEHNQQLLKNVLKLIKKNI GNENAPMWTRIATYTTQIIINSSEBLRDSFL 3471  
Db 3421 GGNHVTMTVAEHNQQLLKNVLKLIKKNI GNENAPMWTRIATYTTQIIINSSEBLRDSFL 3480  
Qy 3472 PLAERYKRTDNMPHKEESLRGFIKSTDDTDSQVESQIOEDWOLLVRDIYSFYPLLLIKYV 3531  
Db 3481 PLAERYKRTDNMPHKEESLRGFIKSTDDTDSQVESQIOEDWOLLVRDIYSFYPLLLIKYV 3540  
Qy 3532 DLQRNHLRNVPABEELYNHVAEIFNIWSKSYFLKEEQNFISANEIDNMVLIIMPTATR 3591  
Db 3541 DLQRNHLRNVPABEELYNHVAEIFNIWSKSYFLKEEQNFISANEIDNMVLIIMPTATR 3600  
Qy 3592 RVTAVTDGTPQGCGKKKKXHRDKKDKXEVQASLWVACLKRLLPVGLNLPAGREQBLVQ 3651  
Db 3601 RVTAVTDGTPQGCGKKKKXHRDKKDKXEVQASLWVACLKRLLPVGLNLPAGREQBLVQ 3660  
Qy 3652 HCKDRP-----LKKMSEQDVAEFAKTQTLTPDKIDPADEMSWOHYLSKLGSKSKSNITV 3706  
Db 3661 HCKDRFLKVGTLKMGSEQDVAEFAKTQTLTPDKIDPADEMSWOHYLSKLGSKSKSNITV 3720  
Qy 3707 ETAENKAKIIDDTVERIVAMSKVLFGHIMIDHPQOMSKNYSRVSVISQIRKRAVIACPRQT 3766  
Db 3721 ETAENKAKIIDDTVERIVAMSKVLFGHIMIDHPQOMSKNYSRVSVISQIRKRAVIACPRQT 3780  
Qy 3767 SLHSLPRHRACNIFARTYYELWLEENIGQEVMIEDLTQSFEDAECLKSDVVEEGEKPD 3826  
Db 3781 SLHSLPRHRACNIFARTYYELWLEENIGQEVMIEDLTQSFEDAECLKSDVVEEGEKPD 3840  
Qy 3827 LTOLVTTFCRGANTERSGALQEDPLVMSVAHIITAKSCGEEBEGGEGGEGGEGGEGG 3886  
Db 3841 LTOLVTTFCRGANTERSGALQEDPLVMSVAHIITAKSCGEEBEGGEGGEGGEGGEGG 3900  
Qy 3887 GRASIEHEQMEKOKLAFHOARLADRGVAEMVLLIHSASKGLPSEMVMKTLQLGSIILRGG 3946  
Db 3901 GRASIEHEQMEKOKLAFHOARLADRGVAEMVLLIHSASKGLPSEMVMKTLQLGSIILRGG 3960  
Qy 3947 NIDIQMGMLNHLKDKXDVGFSTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLSGAAGEKN 4006  
Db 3961 NIDIQMGMLNHLKDKXDVGFSTSIAGLMNSCSVLDLDAFERNTKAEGLGVGLSGAAGEKN 4020  
Qy 4007 MHDAEFTCALFRFIQLTCEGHNLWDQNYLRTQAGNTTNNVITCTVDYLLRLOESIMDFY 4066  
Db 4021 MHDAEFTCALFRFIQLTCEGHNLWDQNYLRTQAGNTTNNVITCTVDYLLRLOESIMDFY 4080  
Qy 4067 WHYSSELIDPAGKANFFKAIQVAVSOVNTLTETVIOGCPCTQNOQALAHSLRWDVAVGGFLF 4126  
Db 4081 WHYSSELIDPAGKANFFKAIQVAVSOVNTLTETVIOGCPCTQNOQALAHSLRWDVAVGGFLF 4140  
Qy 4127 LFSHMQDKLSKHSQVDLLKELLNLQKDMITPMMLSEGNVNGTIGKQWVDTLVESA 4186  
Db 4141 LFSHMQDKLSKHSQVDLLKELLNLQKDMITPMMLSEGNVNGTIGKQWVDTLVESA 4200

QY 4187 VELILKYFDMFLKLDLASSASFOBIDANNQWVLPKDFKEMEQKQSYTPEEIEFLIAC 4246  
Db 4201 VELILKYFDMFLKLDLASSASFOBIDANNQWVLPKDFKEMEQKQSYTPEEIEFLIAC 4260  
QY 4247 CETNHDGKLDYIGFCDRPHEPAKEIGFNLAULLTNLSEHMPNEPLARFLETAGSVLYNF 4306  
Db 4261 CETNHDGKLDYIGFCDRPHEPAKEIGFNLAULLTNLSEHMPNEPLARFLETAGSVLYNF 4320  
QY 4307 EPFLGRIEIMGSKRIERYPEIKESNIQEWEKPOIKESKAPFYYSIVTEGGDKKLEAF 4366  
Db 4321 EPFLGRIEIMGSKRIERYPEIKESNIQEWEKPOIKESKAPFYYSIVTEGGDKKLEAF 4380  
QY 4367 VNFCEDAIFEMTHASGLMAASESVGGTKNREASYMYGDDDDERAGKDPFRRLGQSVD 4426  
Db 4381 VNFCEDAIFEMTHASGLMAASESVGGTKNREASYMYGDDDDERAGKDPFRRLGQSVD 4440  
QY 4427 GVATAFSSLSPSNIAKADMQMPAPBLAVGFFKMPFYLFFYLGYGVLVVVRIFGVLL 4486  
Db 4441 GVATAFSSLSPSNIAKADMQMPAPBLAVGFFKMPFYLFFYLGYGVLVVVRIFGVLL 4500  
QY 4487 GLMRGPQDDEPPPEPEBEKIGQLRHLRLATOSSRHLPALPPADDTGOMQVSAGFLDITK 4546  
Db 4501 GLMRGPQDDEPPPEPEBEKIGQLRHLRLATOSSRHLPALPPADDTGOMQVSAGFLDITK 4560  
QY 4547 EDNGQIQVKPHESPSTSPSSGEEAEVSPDESADHTEQRPPSLDILLGGGQAQKQAOER 4606  
Db 4561 EDNGQIQVKPHESPSTSPSSGEEAEVSPDESADHTEQRPPSLDILLGGGQAQKQAOER 4620  
QY 4607 MEAQAAQQAAMSAIEAESKAVQGPAPALSQVLSQYTRRAVSFLARFNLKVAULV 4666  
Db 4621 MEAQAAQQAAMSAIEAESKAVQGPAPALSQVLSQYTRRAVSFLARFNLKVAULV 4680  
QY 4667 AFCINFVLLFYKVTLDGEGGSGGLDIIAGGSGSGAGSGGSGGSGEGEDDLEVV 4726  
Db 4681 AFCINFVLLFYKVTLDGEGGSGGLDIIAGGSGSGAGSGGSGGSGEGEDDLEVV 4740  
QY 4727 HIDEFFYMEHVIKMAAHLHSIVSLAILIYGYHLKVLPLAIFKREKEIARKLEFDGLYIAE 4786  
Db 4741 HIDEFFYMEHVIKMAAHLHSIVSLAILIYGYHLKVLPLAIFKREKEIARKLEFDGLYIAE 4800  
QY 4787 QPEDDDLKSHWDKLVISAKSPVNVYWDKFKKKVRAKYSYVDFDSISNMLGMEKTSFSA 4846  
Db 4801 QPEDDDLKSHWDKLVISAKSPVNVYWDKFKKKVRAKYSYVDFDSISNMLGMEKTSFSA 4860  
QY 4847 QBEESGKGLIHYIINDRYQWKAGVITIDNSFLYSLWYFSFSGMGNFNFFFAAHLLD 4906  
Db 4861 QBEESGKGLIHYIINDRYQWKAGVITIDNSFLYSLWYFSFSGMGNFNFFFAAHLLD 4920  
QY 4907 VAVGPKTLRTILQSVTHNGKQLVLTVMLLTIIVYTVIAFNFFKFFVYQBEDDEVNRNC 4966  
Db 4921 VAVGPKTLRTILQSVTHNGKQLVLTVMLLTIIVYTVIAFNFFKFFVYQBEDDEVNRNC 4980  
QY 4967 HDMLTCFVFNLYKVRAGGIGDELEPPDGDSEVYRIIFDISFFFFIIVILLAILOGLI 5026  
Db 4981 HDMLTCFVFNLYKVRAGGIGDELEPPDGDSEVYRIIFDISFFFFIIVILLAILOGLI 5040  
QY 5027 IDAFGLRLDQLESVKEDMESNCFICGINKDYFDKVPHPGPDTHVQREHNLANYMFFLMHLI 5086  
Db 5041 IDAFGLRLDQLESVKEDMESNCFICGINKDYFDKVPHPGPDTHVQREHNLANYMFFLMHLI 5100  
QY 5087 NKPDTEYTGQETVYVNMVITQRCWDFPFVGDGCRKQYEDLMGE 5128  
Db 5101 NKPDTEYTGQETVYVNMVITQRCWDFPFVGDGCRKQYEDLMGE 5142

RESULT 4  
US-10-668-767-146  
; Sequence 146, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
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; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BBI533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
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; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 146  
; LENGTH: 5100  
; TYPE: PRT  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; OTHER INFORMATION: pXL-Hv6  
US-10-668-767-146  
  
Query Match 98.9%; Score 26506; DB 4; Length 5100;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 5082; Conservative 5; Mismatches 8; Indels 38; Gaps 3;  
  
QY 1 MAEAGGASEODDVSFLRTEDMVCLSTCTATGERVCLAAEGFGRHCFLENIAADKNIPDDL 60  
Db 1 MAEAGGASEODDVSFLRTEDMVCLSTCTATGERVCLAAEGFGRHCFLENIAADKNIPDDL 60  
QY 61 SOCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILRLHNSDMYL 115  
Db 61 SOCVFVIEQALSVRALQELVTAAGSETKCNLKGTSGHRTLLYGNAILRLHNSDMYL 120  
QY 116 ACLTSSSQDKLAFDVLGLOHQSQGEACWWTLHPASKORSEGEKVRGDDLLILSVATERY 175  
Db 121 ACLTSSSQDKLAFDVLGLOHQSQGEACWWTLHPASKORSEGEKVRGDDLLILSVATERY 180  
QY 176 LHTTKENEVSIVNASFHVTHWSVQPYGTGIRMKYVGVFGDVLRFPHGGDECLTIPST 235  
Db 181 LHTTKENEVSIVNASFHVTHWSVQPYGTGIRMKYVGVFGDVLRFPHGGDECLTIPST 240  
QY 236 WTKDGGQNIYVYEGSVMSQARSRLWRLRLARTKWAGGFINWYHPMRIRHITTGRLGVND 295  
Db 241 WTKDGGQNIYVYEGSVMSQARSRLWRLRLARTKWAGGFINWYHPMRIRHITTGRLGVND 300  
QY 296 QNELYLVSRBATTASCAPLQRBKDDQKQVLEKDLVIGAPIIKYGDSTVIQHSSETG 355  
Db 301 QNELYLVSRBATTASCAPLQRBKDDQKQVLEKDLVIGAPIIKYGDSTVIQHSSETG 360  
QY 356 LMLSVKSVETKKGVKVEEKQAILHBEKGMDGLDPSRSQEBESRTARVIRKCSLFTK 415  
Db 361 LMLSVKSVETKKGVKVEEKQAILHBEKGMDGLDPSRSQEBESRTARVIRKCSLFTK 420  
QY 416 FINGLETLOENRRHSMFFASVNLGEMVNCLEDLINYFAQPDDEMEHEEKQKFRALNRQ 475  
Db 421 FINGLETLOENRRHSMFFASVNLGEMVNCLEDLINYFAQPDDEMEHEEKQKFRALNRQ 480  
QY 476 DLFOEBEGLNLIILBAIDKINIVITSGQFLAGLAGESQSWEMISGYLYQLLAAIKGNH 535  
Db 481 DLFOEBEGLNLIILBAIDKINIVITSGQFLAGLAGESQSWEMISGYLYQLLAAIKGNH 540  
QY 536 TNCAQFANSRLNMLFSLGQASGEGTGMLDVHLCHVLIDSPALNMNRDEHIKVIISLL 595  
Db 541 TNCAQFANSRLNMLFSLGQASGEGTGMLDVHLCHVLIDSPALNMNRDEHIKVIISLL 600  
QY 596 EKHGRDPKVLVDLCSLCVNGVAVRSQNNICDYLPGKNLLQTLVDHVSVPNIFV 655  
Db 601 EKHGRDPKVLVDLCSLCVNGVAVRSQNNICDYLPGKNLLQTLVDHVSVPNIFV 660  
QY 656 GRVGSAYVRKWYFEVTHMDHIEKTHMPHLIRIGWANTTGVYPPGGGKGGVGGDDL 715  
Db 661 GRVGSAYVRKWYFEVTHMDHIEKTHMPHLIRIGWANTTGVYPPGGGKGGVGGDDL 720



Qy	716	YSXFGDGYLWSGGRKTPVNRTHAEEPIIRKGDVIGCALDLTVPIINFMFNGVRVTSFT	775
Db	721	YSYGLDGAYLWSGGRKTPVNRTHAEEPIIRKGDVIGCALDLTVPIINFMFNGVRVTSFT	780
Qy	776	NFNLEGNHFFPVISCSSSKLSRCPLGGHGRHRYAAPEGYSPLVESLPOOILSIEPCFYF	835
Db	781	NFNLEGNHFFPVISCSSSKLSRCPLGGHGRHRYAAPEGYSPLVESLPOOILSIEPCFYF	840
Qy	836	GNLSKRALAGPPLVODDTAFVPTPVDTLQTLPTTYVEQIRDKLAENIHEMWANKIEAGW	895
Db	841	GNLSKRALAGPPLVODDTAFVPTPVDTLQTLPTTYVEQIRDKLAENIHEMWANKIEAGW	900
Qy	896	MYGDQREDLHKIHPCLVPPFERLPPAEKRYDIQLAVQTLKTLALGYVVISLDKPPARINRV	955
Db	901	MYGDQREDLHKIHPCLVPPFERLPPAEKRYDIQLAVQTLKTLALGYVVISLDKPPARINRV	960
Qy	956	RLNPEPMQNSGYKPAFLDSAVTLTPKMBELVDOLAENTHNLWABERIOOGHTYGLNED	1015
Db	961	RLNPEPMQNSGYKPAFLDSAVTLTPKMBELVDOLAENTHNLWABERIOOGHTYGLNED	1020
Qy	1016	SDMHRSPHLYPKVDDAIKKNARDTASETVRTLLVYGYMLDPTTGEQHEALLLEASKQK	1075
Db	1021	SDMHRSPHLYPKVDDAIKKNARDTASETVRTLLVYGYMLDPTTGEQHEALLLEASKQK	1080
Qy	1076	QADPRTYRAEKQYAVSSGKGYFEFEILLTAGPMRVGWAHADMAPGMMLGDQDENSWAEDGYN	1135
Db	1081	QADPRTYRAEKQYAVSSGKGYFEFEILLTAGPMRVGWAHADMAPGMMLGDQDENSWAEDGYN	1140
Qy	1136	EEKYVSGNTSFGQWAGVDVGVFLDLIDKTTISFSLNGELLMDALGGETTADVOGDNF	1195
Db	1141	EEKYVSGNTSFGQWAGVDVGVFLDLIDKTTISFSLNGELLMDALGGETTADVOGDNF	1200
Qy	1196	VPACTGLVGQKARLYTQDQVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWTKDQPIFENT	1255
Db	1201	VPACTGLVGQKARLYTQDQVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWTKDQPIFENT	1260
Qy	1256	DEMIIDTRIDVTRIPAGSDTPCLKISNHTFETMEKANWEFLRLSLPVICNNEFIDEAEKA	1315
Db	1261	DEMIIDTRIDVTRIPAGSDTPCLKISNHTFETMEKANWEFLRLSLPVICNNEFIDEAEKA	1320
Qy	1316	RRWVEIKDRQOILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQBELPSSKMKRLP	1375
Db	1321	RRWVEIKDRQOILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQBELPSSKMKRLP	1380
Qy	1376	SRPFRKSGMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKDKRGRS	1435
Db	1381	SRPFRKSGMTR-----GQVNGMHRSTSEAEMAKYDLGAQGLTPDDKDKRGRS	1428
Qy	1436	PFKPFRRKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNPOIKVSOANQRYNGHNA	1495
Db	1429	PFKPFRRKRGESSDRAKSRKSTPDPFSDTEVSPERGARRPNPOIKVSOANQ-----	1481
Qy	1496	PSRTNLVGSQVGLNMAPTDORUKOMTSTLLAQSAATEVGNNEIPDAECLKLINEFYGVRI	1555
Db	1482	-----MAPTDORUKOMTSTLLAQSAATEVGNNEIPDAECLKLINEFYGVRI	1527
Qy	1556	YPGQDPHTHVIGWYTTQYHLHSKDFNOSKVTKSSVIIITDDYDRVVENNVNQSCVMRADE	1615
Db	1528	YPGQDPHTHVIGWYTTQYHLHSKDFNOSKVTKSSVIIITDDYDRVVENNVNQSCVMRADE	1587
Qy	1616	LYNEVMAEATKAGASQGMFICGSYDVTSTGVSFTCEGKOTSFPEKMEPETKLPAAIPEVA	1675
Db	1588	LYNEVMAEATKAGASQGMFICGSYDVTSTGVSFTCEGKOTSFPEKMEPETKLPAAIPEVA	1647
Qy	1676	TSKEILOELGRSATSPLSAAVLPTSDXKVIPOFPPLRLKVCQILKPHQWAVRPNQSLQVH	1735
Db	1648	TSKEILOELGRSATSPLSAAVLPTSDXKVIPOFPPLRLKVCQILKPHQWAVRPNQSLQVH	1707
Qy	1736	ALKLUSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLUSFHSHTLTLYAALCYQ	1795
Db	1708	ALKLUSDIRGWSMLCEDAVSMLALHIPEDRCIDILEPIEMDKLUSFHSHTLTLYAALCYQ	1767

[illegible]

2848 Db GEGSDSQKTHPRLKPYNNLNDYEKERYKEPVRESLKALLAIGVSEHSEVDIESNNRSS 2907  
2936 QY MRRQSKSGRPEIIVTDSATFPDYNPHVDVNTNLTLSREMOMAEERADNAHD1WAKKK 2995  
2908 Db MRRQSKSGRPEIIVTDSATFPDYNPHVDVNTNLTLSREMOMAEERADNAHD1WAKKK 2967  
2996 QY EELVTNGGIIHPQVLPVYDOLLTDKEKKDRERSQEFKYLQYQGYKLRHPSKAPQSDTEQT 3055  
2968 Db EELVTNGGIIHPQVLPVYDOLLTDKEKKDRERSQEFKYLQYQGYKLRHPSKAPQSDTEQT 3027  
3056 QY TTGVAIELRFAYSLEKLIQVIDRATINMKLLKPSITFSRRSSPKTSTRDIKFFSKAVLP 3115  
3028 Db TTGVAIELRFAYSLEKLIQVIDRATINMKLLKPSITFSRRSSPKTSTRDIKFFSKAVLP 3087  
3116 QY LMKEYFSTRHNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSLAFAFGPDVRTV 3175  
3088 Db LMKEYFSTRHNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSLAFAFGPDVRTV 3147  
3176 QY RCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITIMNLQDKYAHLRGTHLKT 3235  
3148 Db RCLQVLVKGIDAKSLVKNCPEFIRTSMLTFFNNVADDVGHITIMNLQDKYAHLRGTHLKT 3207  
3236 QY STSLGYINGVLLPILITAKFDHLANCEYGADLLDLDEIQVASYKMLGSLYALGTDASLTHDR 3295  
3208 Db STSLGYINGVLLPILITAKFDHLANCEYGADLLDLDEIQVASYKMLGSLYALGTDASLTHDR 3267  
3296 QY KYLKTEIERHHPALGSCLGAFSSPPVAFLEPHLNKQNFSLNRIADHSLEAQDIMQNM 3355  
3268 Db KYLKTEIERHHPALGSCLGAFSSPPVAFLEPHLNKQNFSLNRIADHSLEAQDIMQNM 3327  
3356 QY EOCMPTLETILGEVDQFVESDKTYNEAPHIIDVLPCLCSYLPFWAAGPDNVTPTGNGH 3415  
3328 Db EOCMPTLETILGEVDQFVESDKTYNEAPHIIDVLPCLCSYLPFWAAGPDNVTPTGNGH 3387  
3416 QY VTMVTAEHMQLKNVLLKIKKNIKENAPWMTRIATYTOQIIINSSEELRDSFLPLAE 3475  
3388 Db VTMVTAEHMQLKNVLLKIKKNIKENAPWMTRIATYTOQIIINSSEELRDSFLPLAE 3447  
3476 QY RVRKRTDNMFKEESLRGFIKSTDDTSQVESQIQEDWQLLVRIYSPYLLIKYVDLQR 3535  
3448 Db RVRKRTDNMFKEESLRGFIKSTDDTSQVESQIQEDWQLLVRIYSPYLLIKYVDLQR 3507  
3536 QY NHWLRNNVPEABELNHNVAEIPNIWSKQYFLKEQNEFISANEIDNMVLIIMPTATRRVTA 3595  
3508 Db NHWLRNNVPEABELNHNVAEIPNIWSKQYFLKEQNEFISANEIDNMVLIIMPTATRRVTA 3567  
3596 QY VTDGTPQGGKKKKKHKRDKRDKKEVQASLMVACLKELLPVGLNLFAGREOELVQHCKD 3655  
3568 Db VTDGTPQGGKKKKKHKRDKRDKKEVQASLMVACLKELLPVGLNLFAGREOELVQHCKD 3627  
3656 QY RFLKQMSQDVAEFAKTQTLTPDKIDPADEMSWOHLYSKLGSKSKSNIITVETAENKAKI 3715  
3628 Db RFLKQMSQDVAEFAKTQTLTPDKIDPADEMSWOHLYSKLGSKSKSNIITVETAENKAKI 3687  
3716 QY IDDTVERIVAMSKVLPGLHMDHPQMSKNVYRSVVS1QRKRAVTACERQTSLSLSPRHR 3775  
3688 Db IDDTVERIVAMSKVLPGLHMDHPQMSKNVYRSVVS1QRKRAVTACERQTSLSLSPRHR 3747  
3776 QY ACNIFARTYVELWLEENIGQWMLIDLTSQPEDAELKSDVVEGEKPDPLTQLVTTF 3835  
3748 Db ACNIFARTYVELWLEENIGQWMLIDLTSQPEDAELKSDVVEGEKPDPLTQLVTTF 3807  
3836 QY RGAMTERSALQEDPLYMSYAHIIAKSCGEEEBEGGEBEGGABAEDEGRASIHQOE 3895  
3808 Db RGAMTERSALQEDPLYMSYAHIIAKSCGEEEBEGGEBEGGABAEDEGRASIHQOE 3867  
3896 QY MEKQKLLFHOARLADRGVAEMVLLHISAKGILPSEMWNKTIOLG1SILRGGNID1OMGNL 3955  
3868 Db MEKQKLLFHOARLADRGVAEMVLLHISAKGILPSEMWNKTIOLG1SILRGGNID1OMGNL 3927  
3956 QY NHLKDKKDVGFFTSIAGLMNCSVLDDAFERNTKAEGLVGLEGAAGEKNMHDAEFTCA 4015

3928 Db NHLKDKKDVGFFTSIAGLMNCSVLDDAFERNTKAEGLVGLEGAAGEKNMHDAEFTCA 3987  
4016 QY LRFPIQLTCEGHNLDMQNYLRTQAGNTTTNNVVICITVDYLLRLQOESIMDFYHYSKELI 4075  
3988 Db LRFPIQLTCEGHNLDMQNYLRTQAGNTTTNNVVICITVDYLLRLQOESIMDFYHYSKELI 4047  
4076 QY DPAGKANFFKAIGVASQVFNTLITEVIOGPTCQNOQAALAHSLRLMDAVGGFPLPFSHMODKL 4135  
4048 Db DPAGKANFFKAIGVASQVFNTLITEVIOGPTCQNOQAALAHSLRLMDAVGGFPLPFSHMODKL 4107  
4136 QY SKHSSQVDDLKELNLKQDMI PMWLSMLEGNVNGTIGKQWVDTLVESASNVLELILKYFD 4195  
4108 Db SKHSSQVDDLKELNLKQDMI PMWLSMLEGNVNGTIGKQWVDTLVESASNVLELILKYFD 4167  
4196 QY MFLKLDLTSASFOEIDANNMGVLPKDKFKEKMEQKSYTPBIEIFLLACCTNHGDKL 4255  
4168 Db MFLKLDLTSASFOEIDANNMGVLPKDKFKEKMEQKSYTPBIEIFLLACCTNHGDKL 4227  
4256 QY DYIGFCDRFHEPAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNVPEPFLGRIEI 4315  
4228 Db DYIGFCDRFHEPAKEIGFNLAVALLTNLSEHMPNEPRLARFLETAGSVLNVPEPFLGRIEI 4287  
4316 QY MGSKRIERYVFEIKESNIEBQWEKPOIKESKRAFFYSIVTTEGGDKEXLEAFVNFCEDAIF 4375  
4288 Db MGSKRIERYVFEIKESNIEBQWEKPOIKESKRAFFYSIVTTEGGDKEXLEAFVNFCEDAIF 4347  
4376 QY EMTHASGLMAASBESVGGTKNREASYMYMGDDDDERAGKOPFRRLGLOSKVGATAFSSL 4435  
4348 Db EMTHASGLMAASBESVGGTKNREASYMYMGDDDDERAGKOPFRRLGLOSKVGATAFSSL 4407  
4436 QY SPSNIAKIAIDMQMPPAEALAVGFFKMFYLYFYLYGYGVLVVRYIIFGVLLGLMRGPOTD 4495  
4408 Db SPSNIAKIAIDMQMPPAEALAVGFFKMFYLYFYLYGYGVLVVRYIIFGVLLGLMRGPOTD 4467  
4496 QY EPPPEPTEEBEIKGOLRRLRLATQSSRLHPALPPADDTGOMQVSAFGDITKEDNGQIOVK 4555  
4468 Db EPPPEPTEEBEIKGOLRRLRLATQSSRLHPALPPADDTGOMQVSAFGDITKEDNGQIOVK 4527  
4556 QY PHEPSPSTSPSSGEEAEVSPDESADHTEBOQPPSLIDLLGGEQAKQAQERMEAAQAA 4615  
4528 Db PHEPSPSTSPSSGEEAEVSPDESADHTEBOQPPSLIDLLGGEQAKQAQERMEAAQAA 4587  
4616 QY AMSAIEAESKKAQVGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLL 4675  
4588 Db AMSAIEAESKKAQVGPAPSALSQVDLSQYTRRAVSFLARNFYNLKYVALVLAFCINFVLL 4647  
4676 QY FYKVSTLDEGEGSGGLGDIIAGGSGSGAGSGSGSGSGEDDDALEVVHIDEDFFVM 4735  
4648 Db FYKVSTLDEGEGSGGLGDIIAGGSGSGAGSGSGSGSGEDDDALEVVHIDEDFFVM 4707  
4736 QY EHVIMKMAVLHSIVSLAILIGYVHLKVPALAIKREKEIARKLEPDGLYIAEQPEDDDLLKS 4795  
4708 Db EHVIMKMAVLHSIVSLAILIGYVHLKVPALAIKREKEIARKLEPDGLYIAEQPEDDDLLKS 4767  
4796 QY HWDKLVISAKSPFVNYNDKFKVKKVRAKYSITYDFDSISNMLGMEKTSFSQAEEBSGKGL 4855  
4768 Db HWDKLVISAKSPFVNYNDKFKVKKVRAKYSITYDFDSISNMLGMEKTSFSQAEEBSGKGL 4827  
4856 QY IHYIINIDWRVQVWKAGVTITDNSFLYSMTWFSVSMGNFNFPFAAHLLDVAVGPKTLR 4915  
4828 Db IHYIINIDWRVQVWKAGVTITDNSFLYSMTWFSVSMGNFNFPFAAHLLDVAVGPKTLR 4887  
4916 QY TILOSVTHNGKQLVLTVMLLTIIIVYITVIAFNFRKPYVOEEDDEVNRNCHMDLTCFVF 4975  
4888 Db TILOSVTHNGKQLVLTVMLLTIIIVYITVIAFNFRKPYVOEEDDEVNRNCHMDLTCFVF 4947  
4976 QY NLYKXVRAGGIGDELEPPDGDSEVYRIIFDIISFFPFIIVILLAILQGLIIDAFGEURD 5035  
4948 Db NLYKXVRAGGIGDELEPPDGDSEVYRIIFDIISFFPFIIVILLAILQGLIIDAFGEURD 5007  
5036 QY QLESVKEDMESNCFICGINKOYFDKVPHGFDTHVQREHNLANYPFMLHMLINKPDTEYTG 5095  
5008 Db QLESVKEDMESNCFICGINKOYFDKVPHGFDTHVQREHNLANYPFMLHMLINKPDTEYTG 5067

Qy 5096 QETVWNNYTORCWDFPVPVGVGCFRQKQYEDLNGE 5128  
Db 5068 QETVWNNYTORCWDFPVPVGVGCFRQKQYEDLNGE 5100

RESULT 5

US-10-668-767-2  
; Sequence 2, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BBI533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668.767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 5142  
; TYPE: PRT  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1755)..(1755)  
; OTHER INFORMATION: Xaa = Ser  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4250)..(4250)  
; OTHER INFORMATION: Xaa = Thr  
US-10-668-767-2

Query Match 98.8%; Score 26469; DB 4; Length 5142;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 5074; Conservative 18; Mismatches 36; Indels 14; Gaps 3;  
Qy 1 MAEAGGASEDDVSFLRTEDMVCISCTATGERVCLAAEGFGRHCFLENTADKNIPDL 60  
Db 1 MAEAGGASEDDVSILRTEDMVCISCTATGERVCLAAEGFGRHCFLENTADKNIPDL 60  
Qy 61 SQCVFVIRQALSVRALQELVTAAGSET-----GKGTGSGHRTLTYGNAILLRHLSNMYL 115  
Db 61 SQCVFVIRQALSVRALQELVTAAGSETKENLKGTSGYRTLTYGNAILLRHLSNMYL 120  
Qy 116 ACLTSSSQDKLAFDVLGLOQHSQGEACWTLHPASQORSEGEKVRVGDDLLILSVATERY 175  
Db 121 ACLTSSSQDKLAFDVLGLOQHSQGEACWTLHPASQORSEGEKVRVGDDLLILSVATERY 180  
Qy 176 LHHTKENEVSIVNASFVHTWSVQPYGTGIRSMKYGVVFGDVLRFPHGGDECLTTPST 235  
Db 181 LHHTKENEVSIVNASFVHTWSVQPYGTGIRSMKYGVVFGDVLRFPHGGDECLTTPST 240  
Qy 236 WTKDGGQNI VYVYEGGSVMSQARSRLRLRLATKRWAGGF INWYHPMRIRHITTYGRYLVND 295  
Db 241 WTKDGGQNI VYKGSVMSQARSRLRLRLATKRWAGGF INWYHPMRIRHITTYGRYLVND 300  
Qy 296 QNELYLVSREBATTASCAFLRQEKDDQVLEKDKLEIVIGAPIIKYGDSTVI VQHSETG 355  
Db 301 QNELYLVSREBPTTASCAFLRQEKDDQVLEKDKLEIVIGAPIIKYGDSTVI VQHSETG 360  
Qy 356 LWLSYKSYETKKGVKVEEQAILHBECKWDDGLDPSRQSEESRTARVIRKCSSLFTK 415  
Db 361 LWLSYKSYETKKGVKVEEQAILHBECKWDDGLDLSRSQSEESMTARVIRKCSSLFTK 420

Qy 416 FINGLETQENRRHSMPFASVNLGEMVMCLDLINYPAQDPEDEMEHEEKONKFRALNRQ 475  
Db 421 FINGLETQENRRHSMPFASVNLGEMVMCLDLINYPAQDPEDEMEHEEKONKFRALNRQ 480  
Qy 476 DLFOEGILNLILEADKINVTISQGFAGFLAGDESQGSWEMISGYLYQLLAAIIKGNH 535  
Db 481 DLFOEGILNLILEADKINVTISQGFAGFLAGDESQGSWEMISGYLYQLLAAIIKGNH 540  
Qy 536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPALNNMRDEHIKVIISLL 595  
Db 541 TNCAQFANSNRFNWLSRLGSQASGEGTGMLDVLHCVLIDSPALNNMRDEHIKVIISLL 600  
Qy 596 EKHGRDPKVL DVLCSLCVGVNGVAVRSQNNICDYLPGKNLLIQTALVDHVSVRPNI FV 655  
Db 601 EKHGRDPKVL DVLCSLCVGVNGVAVRSQNNICDYLPGKNLLIQTALVDHVSVRPNI FV 660  
Qy 656 GRVGSNAVYRKWYFEVTMDHIEKTHMMPHLRIGWANTTGYVPYGGGKGWGVGDDDL 715  
Db 661 GRVGSNAVYRKWYFEVTMDHIEKTHMMPHLRIGWANTTGYVPYGGGKGWGVGDDDL 720  
Qy 716 YSYGFDGAYLWSGGRKTPVNRTHAEBPYIRKGDVIGCALDLTVPIINFMFNGVRVTSFT 775  
Db 721 YSYGFDGAYLWSGGRKTPVNRTHAEBPYIRKGDVIGCALDLTVPIINFMFNGVRVTSFT 780  
Qy 776 NFNLEGMFPFVISCSSKLSRFLGGEHGLRVAABEGYSPLVESLLPQOILSLEPCFYF 835  
Db 781 NFNLEGMFPFVISCSSKLSRFLGGEHGLRVAABEGYSPLVESLLPQOILSLEPCFYF 840  
Qy 836 GNLKRALAGPPLVQDDTAFVPTPVDLQITLTYVEQIRDKLAENIHEMWNMKIEAGW 895  
Db 841 GNLKRALAGPPLVQDDTAFVPTPVDLQITLTYVEQIRDKLAENIHEMWNMKIEAGW 900  
Qy 896 MYGDQREDLHKIHPCLVPPFERLPPAEKRYDIAVQTLTKTILALGYVISLDKPPARINV 955  
Db 901 MYGDQREDLHKIHPCLVPPFERLPPAEKRYDIAVQTLTKTILALGYVISLDKPPARINV 960  
Qy 956 RLPNEPQMONGYKAPLDLSAVTLTPQMDLVQDLAENHNLWARERI OOGWTYGLNED 1015  
Db 961 RLPNEPQMONGYKAPLDLSAVTLTPQMDLVQDLAENHNLWARERI OOGWTYGLNED 1020  
Qy 1016 SDMHRSPHLVPYPKVDDDAIKKANRDPTASEVTRTLLVYGYMLDPTTQGEHALLLEASKQK 1075  
Db 1021 SDMHRSPHLVPYPKVDDDAIKKANRDPTASEVTRTLLVYGYMLDPTTQGEHALLLEASKQK 1080  
Qy 1076 QADFRTRYAEKNYAVSSGKWYFEFEILLTAGPMRVGAHADMAFGMMLGQDENSWAFPGYN 1135  
Db 1081 QADFRTRYAEKNYAVSSGKWYFEFEILLTAGPMRVGAHADMAFGMMLGQDENSWAFPGYN 1140  
Qy 1136 EEKYSGNTESFGKQWAGDVGVFLDLIDKTTISFSLNGELLMDALGGETTADVOGDNF 1195  
Db 1141 EEKYSGNTESFGKQWAGDVGVFLDLIDKTTISFSLNGELLMDALGGETTADVOGDNF 1200  
Qy 1196 VPACTLGVGQKARLTYGQDVNTILKYFTTCGLQGYBPFVNMKRDVTHWTYTKDQPIFENT 1255  
Db 1201 VPACTLGVGQKARLTYGQDVNTILKYFTTCGLQGYBPFVNMKRDVTHWTYTKDQPIFENT 1260  
Qy 1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTPETMEKANWEFLRSLPVI CHNEFIDEAEKA 1315  
Db 1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTPETMEKANWEFLRSLPVI CHNEFIDEAEKA 1320  
Qy 1316 RRWVEIKDRQOILMKEAVEAQMPAHIDQIMRSGFTWMDIKGLHYEDNQEBLPSSMKRLP 1375  
Db 1321 RRWVEIKDRQOILMKEAVEAQMPAHIDQIMRSGFTWMDIKGLHYEDNQEBLPSSMKRLP 1380  
Qy 1376 SRPFRKSGMTRGVTIONYNNLQPGVNGMHRSTSEAEKAYDLGAQGLTPDDKKDKRGSR 1435  
Db 1381 SRPFRKSGMTRGVTIONYNNLQPGVNGMHRSTSEAEKAYDLGAQGLTPDDKKDKRGSR 1440  
Qy 1436 PFKFRKSGESSDRAKRSKTPDPFSDTEVSPERGARPENQIKVYSQANQRVNGNAR 1495  
Db 1441 PFKFRKSGESSDRAKRSKTPDPFSDTEVSPERGARPENQIKVYSQANQRVNGNAR 1500



QY 1496 PSRTNLQSGVGLN-----MATPTODRKQMTTSTLAQSAATETVGNIEFPAECLKLINEYFY 1551  
Db 1501 PSRTNLQSGVGLNSNAQWATPTODRKQMTTSTLAQSAATETVGNIEFPAECLKLINEYFY 1560  
QY 1552 GVRYYPGQDPHTVYIGWYTTQYHLHSKDPNQS KVTKSSVITDDYDRVVENVNRQSCYV 1611  
Db 1561 GVRYYPGQDPHTVYIGWYTTQYHLHSKDPNQS KVTKSSVITDDYDRVVENVNRQSCYV 1620  
QY 1612 RADELYNEVMAEATAKAGSQGMFICGSVDYTGVSFTCEGKDTSPFKEMPEPKLPAPAI 1671  
Db 1621 RADELYNEVMAEATAKAGSQGMFICGSVDYTGVSFTCEGKDTSPFKEMPEPKLPAPAI 1680  
QY 1672 FVEATSKELIQIELGRSATSPLSAVLPTSDKHVIPPFPRLKVCQCLPKHQWARPVQNS 1731  
Db 1681 SVEATSKELIQIELGRSATSPLSAVLPTSDKHVIPPFPRLKVCQCLPKHQWARPVQNS 1740  
QY 1732 LQVHALKLSDRGWSMLCEDAVSMALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791  
Db 1741 LQVHALKLSGIRGWMLCEDAVSMALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1800  
QY 1792 LCYQSNYRAAHALCTHVDOKOLLYAIQSOYMSGRLRQGFYDLIALHLESHATTMEACKN 1851  
Db 1801 LCYQSNYRAAHALCALSHADOKOLLYAIQSOYMSGRLRQGFYDLIALHLESHATTMEACKN 1860  
QY 1852 EFVIFLGPPELKALYEEDPMGHSLRSLOTESVVRPQMKMTDIAESITEISNLISPYPPLEVA 1911  
Db 1861 EFVIFLGPPELKALYEEDPMGHSLRSLOTESVVRPQMKMTDIAESITEISNLISPYPPLEVA 1920  
QY 1912 REFVMAALAEAVETQVNRDVPVGSNENLFUPLIKLVDRLLVGMWDEDEVEKLLIMTN 1971  
Db 1921 REFVMAALAEAVETQVNRDVPVGSNENLFUPLIKLVDRLLVGMWDEDEVEKLLIMTN 1980  
QY 1972 PETWDPSPDKEGDEHRKGLLHMKAEGAKLQMCVLLQHLNDIQLRHVEATIAFAHDFV 2031  
Db 1981 PETWDPSPDKEGDEHRKGLLHMKAEGAKLQMCVLLQHLNDIQLRHVEATIAFAHDFV 2040  
QY 2032 GLOQTDLQRLRYTEIKOSDLPASAANKTREFCPCPREQMNAILSPKHLSEEDKENCPCGE 2091  
Db 2041 GLOQTDLQRLRYTEIKOSDLPASAANKTREFCPCPREQMNAILSPKHLSEEDKENCPCGE 2100  
QY 2092 ELIARMEFHDTLMAHVSILHALQEPDAAENQBPPEAKPGAFGLYNIINTVKELEBEAKAI 2151  
Db 2101 ELIARMEFHDTLMAHVSILHALQEPDAAENQBPPEAKPGAFGLYNIINTVKELEBEAKAI 2160  
QY 2152 EBPBKKTPEKPKRVLIQTIIVNABESQIETPKLVREMPSSLVROYDVGELIRALEKTY 2211  
Db 2161 EBPBKKTPEKPKRVLIQTIIVNABESQIETPKLVREMPSSLVROYDVGELIRALEKTY 2220  
QY 2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQBEELMRKELWKLNNHTFFQHPDLIRVLR 2271  
Db 2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQBEELMRKELWKLNNHTFFQHPDLIRVLR 2280  
QY 2272 VHENVMAVMNTLGRRAQAQSDAQSPSSQPVASDSKEKDTSHEMVACCRFLCYFCRTGRQ 2331  
Db 2281 VHENVMAVMNTLGRRAQAQSDAQSPSSQPVADNKEKDTSHEMVACCRFLCYFCRTGRQ 2340  
QY 2332 NQKAMFDPHDFLLENSNILLRSPSLRGSTPLDVAYSSMLMENTELALAREHYLEKIAVYL 2391  
Db 2341 NQKAMFDPHDFLLENSNILLRSPSLRGSTPLDVAYSSMLMENTELALAREHYLEKIAVYL 2400  
QY 2392 SRCGLQSNSELYEKGYPDIGWDPVEGERYLDLRFVCMVNGSVESVENANLVRLLIRPE 2451  
Db 2401 SRCGLQSNSELYEKGYPDIGWDPVEGERYLDLRFVCMVNGSVESVENANLVRLLIRPE 2460  
QY 2452 CLGPALRGEGELLKAIIVANKMSERIAADRRLKREMEQGDVNFSPHLPESDEDEDYIDT 2511  
Db 2461 CLGPALRGEGELLKAIIVANKMSERIAADRRLKREMEQGDVNFSPHLPESDEDEDYIDT 2520  
QY 2512 GAAILNFYCTLVDLLGRCAPDAGVIALGNESILRAAILRSVLPLEDLQGLVSLRFTLNN 2571  
Db 2521 GAAILNFYCTLVDLLGRCAPDAGVIALGNESILRAAILRSVLPLEDLQGLVSLRFTLNN 2580  
QY 2572 PAAGEERPKSDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLBEAFPLDRLRAATMLDR 2631

Db 2581 PAAGEERPKSDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLBEAFPLDRLRAATMLDR 2640  
QY 2632 NDGCESDMALSMNRYIGNSLIPLLIKHAYFNEAENYASLLDALHTVYRLSKNRMILTKG 2691  
Db 2641 NDGCESDMALSMNRYIGNSLIPLLIKHAYFNEAENYASLLDALHTVYRLSKNRMILTKG 2700  
QY 2692 QREAVSDFLVALTSAMQPSMLLKLRLKTVDVSKLSEYTTVALRLTLHYERCACKYVYST 2751  
Db 2701 QREAVSDFLVALTSAMQPSMLLKLRLKTVDVSKLSEYTTVALRLTLHYERCACKYVYST 2760  
QY 2752 GAGGAGFASGASDEBKRLTMMLFNSIFDLSKMDYEPFLFGKALPCLLTAIGCALPPDYLS 2811  
Db 2761 GAGGAGFASGASDEBKRLTMMLFNSIFDLSKMDYEPFLFGKALPCLLTAIGCALPPDYLS 2820  
QY 2812 KNYDDEYFGKEQAAGDLNDPOYDPOPIINTSSVALNNDLNTIVQKFSHYHDAWASKRIEN 2871  
Db 2821 KNYDDEYFGKEQAAGDLNDPOYDPOPIINTSSVALNNDLNTIVQKFSHYHDAWASKRIEN 2880  
QY 2872 GWYTGEGWSDSQKTHPRLKPNMMLNDYKERYKEPVRESLKALLAIAGWSVEHSEVDIPSN 2931  
Db 2881 GWYTGEGWSDSQKTHPRLKPNMMLNDYKERYKEPVRESLKALLAIAGWSVEHSEVDIPSN 2940  
QY 2932 NRSSMRQSKSGRPPPEIVTDSATPFYNPHVPDMTNLTLSREMNMAERLADNAHDIA 2991  
Db 2941 NRSSMRQSKSGRPPPEIVTDSATPFYNPHVPDMTNLTLSREMNMAERLADNAHDIA 3000  
QY 2992 KKKKEELVTNGGGIHPOLVPYDILLTDKEKKKDRSOFELKLYOVQYKLRHPSKAPOSD 3051  
Db 3001 KKKKEELVTNGGGIHPOLVPYDILLTDKEKKKDRSOFELKLYOVQYKLRHPSKAPOSD 3060  
QY 3052 TEQTTTGVAILERFAYSILLEKLIQYIDRATINMKLLKPPSTTFSRRSSPKTSTRIDIKFFSK 3111  
Db 3061 TEQTTTGVAILERFAYSILLEKLIQYIDRATINMKLLKPPSTTFSRRSSPKTSTRIDIKFFSK 3120  
QY 3112 AVLPLMEKYFSTHRNYFIAVATATNNVGAASLKEKEMVAALFCKLASLLRSLAAGFQDV 3171  
Db 3121 VVPLMEKYFSTHRNYFIAVATATNSVGAASLKEKEMVAALFCKLASLLRSLAAGFQDV 3180  
QY 3172 RITVRCLQVLVKGIDAKSLVKNCPEFRTSMLTFFNNVADDVGHITIMLQDKYVAHLRGT 3231  
Db 3181 RITVRCLQVLVKGIDAKSLVKNCPEFRTSMLTFFNNVADDVGHITIMLQDKYVAHLRGT 3240  
QY 3232 HLKTSLSGYINGVLLPILITAKFDHLANCEYAGDLLLDEIQVASYKMLGSLYALGTDSL 3291  
Db 3241 HLKTSLSGYINGVLLPILITAKFDHLANCEYAGDLLLDEIQVASYKMLGSLYALGTDSL 3300  
QY 3292 THDRKYLKTEIERHKPALGSCIGAFSPFPVAFLEPHLNKINQPSLLNRIADHSLAEOI 3351  
Db 3301 THDRKYLKTEIERHKPALGSCIGAFSPFPVAFLEPHLNKINQPSLLNRIADHSLAEOI 3360  
QY 3352 MQKMEQCHPTLETITLGEVDQFVESDKTYNEAPHIIDVVLPLLCVLPFWMAQGPNDVPT 3411  
Db 3361 MQKMEQCHPTLETITLGEVDQFVESDKTYNEAPHIIDVVLPLLCVLPFWMAQGPNDVPT 3420  
QY 3412 GGNHVVTYTAHNMOLLKANVLKIKKIGNENAPMWTIATVTOOIIINSSEELLRDSFL 3471  
Db 3421 GGNHVVTYTAHNMOLLKANVLKIKKIGNENAPMWTIATVTOOIIINSSEELLRDSFL 3480  
QY 3472 PLAERVRKRTDNMFHKEESLRGFIKSTDDTSQVESQIOEDWQLLVROIYSPYPLLIKYV 3531  
Db 3481 PLAERVRKRTDNMFHKEESLRGFIKSTDDTSQVESQIOEDWQLLVROIYSPYPLLIKYV 3540  
QY 3532 DLQRNHWLRNVNPEABELYNHVAEIFNIWKSQYFLKEEQNFISANEIDNMVLIIMPATR 3591  
Db 3541 DLQRNHWLRNVNPEABELYNHVAEIFNIWKSQYFLKEEQNFISANEIDNMVLIIMPATR 3600  
QY 3592 RVTAVTGDTPOGGGKKKKKRDKDKDKEVQASLMVACLKRLLPVGLNLFAGRQELVQ 3651  
Db 3601 RVTAVTGDTPOGGGKKKKKRDKDKDKEVQASLMVACLKRLLPVGLNLFAGRQELVQ 3660  
QY 3652 HCKDRF-----LKKMSEQDVAEFAKTQTLTLPDKIDPADEMSMQHYLSKLGSKSNITV 3706

Db 3661 HKDRFLKVGTLKKMSQDVAEFAKTQLTLPDKIDPADMSQHYLSKLGSKSKSNITV 3720  
Qy 3707 ETAENKAKIIDDVTVERIVANSKVLFGLLHMDHPQMSKNVYRSVVSQRKRAVITACFRQT 3766  
Db 3721 ETAENKAKIIDDVTVERIVANSKVLFGLLHMDHPQMSKNVYRSVVSQRKRAVITACFRQT 3780  
Qy 3767 SLHSLPHRRACNIIFARTYYELWLBEENIQBWMLIEDLTQSPEDAELKKSDDVVEGEKPD 3826  
Db 3781 SLHSLPHRRACNIIFARTYYELWLBEENIRQBWMLIEDLTQSPEDAELKKSDDVVEGEKPD 3840  
Qy 3827 LTQLVTTFCRGAMTERSALQEDPLYMSYAHIIAKSCGEEBEGGEBEGGGBAEAEDE 3886  
Db 3841 LTQLVTTSCRGAMTERSALQEDPLYMSYAHIIAKSCGEEBEGGEBEGGGBAEAEDE 3900  
Qy 3887 GRASIHQEMEKQKLLFHOARLADRGVAEMVLLHHISAKGLPSPVMWKTQLGSIILRG 3946  
Db 3901 GRASIHQEMEKQKLLFHOARLADRGVAEMVLLHHISAKGLPSPVMWKTQLGSIILRG 3960  
Qy 3947 NIDIQMGMLNHLKDKKQDVGFPTSAGLMNSCSVLDDAFERNTKABGLGVGLEGAAGEKN 4006  
Db 3961 NIDIQMGMLNHLKDKKQDVGFPTSAGLMNSCSVLDDAFERNTKABGLGVGLEGAAGEKN 4020  
Qy 4007 MHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTIVNVVICTVDYLLRLQBSIMDFY 4066  
Db 4021 MHDAEFTCALFRFIQLTCEGHNLDWQNYLRTQAGNTTIVNVVICTVDYLLRLQBSIMDFY 4080  
Qy 4067 WHYSKELIDPAGKANFFKALGVASQVNTLTETVIOGPCTONQOALAHSLRWDVAGGFLF 4126  
Db 4081 WHYSKELIDPAGKANFFKALGVASQVNTLTETVIOGPCTONQOALAHSLRWDVAGGFLF 4140  
Qy 4127 LFSHQMDKLSKHSSQVLLKELLNLOKDMI PMMLSMLEGNVNGTIGQMWYDTLVESASN 4186  
Db 4141 LFSHQMDKLSKHSSQVLLKELLNLOKDMI PMMLSMLEGNVNGTIVKQWVDTLVGSASN 4200  
Qy 4187 VELILKYFDMFLKLDLTSSAFQIDANNDGWLPKDFKEMEQKSYTPPEIEFLFLLAC 4246  
Db 4201 VELILKYFDMFLKLDLTSSAFQIDANNDGWLPKDFKEMEQKSYTPPEIEFLFLLAC 4260  
Qy 4247 CETNHDGKLDYIGCDRPHPEAKAIGFNVLAVLLTNLSEHMNEPRLARFLETAGSVLYNP 4306  
Db 4261 CETNHDGKLDYIGCDRPHPEAKAIGFNVLAVLLTNLSEHMNEPRLARFLETAGSVLYNP 4320  
Qy 4307 EPFLGRIBMGSKRIERYVEIIESNEIOEKEQIKESKRAFFYSIVTEGGDEKLEAF 4366  
Db 4321 EPFLGRIBMGSKRIERYVEIIESNEIOEKEQIKESKRAFFYSIVTEGGDEKLEAF 4380  
Qy 4367 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRLQSVKD 4426  
Db 4381 VNFCEDAIFEMTHASGLMAASEESVGGTKNREASYMYMGDDDDERAGKDPFRRLQSVKD 4440  
Qy 4427 GVATAFSSLSNIAKADIADQMPAPLAVGFFKMFYLYLYGYGLVWVRYIFGVLL 4486  
Db 4441 GVATAFSSLSNIAKADIADQMPAPLAVGFFKMFYLYLYGYGLVWVRYIFGVLL 4500  
Qy 4487 GLMRGPOTDEPPPEETEEKIGQLRHRLATQSSRHLPALPPADDTGQMVSARGLDITK 4546  
Db 4501 GLMRGPOTDEPPPEETEEKIGQLRHRLATQSSRHLPALPPADDTGQMVSARGLDITK 4560  
Qy 4547 EDNGQIQVKPHESPTSTPSSGGEAEVSPDSADHTEQRPPSLIDLIGGEQAQKQOER 4606  
Db 4561 EDNGQIQVKPHESPTSTPSSGGEAEVSPDSADHTEQRPPSLIDLIGGEQAQKQOER 4620  
Qy 4607 MEAQAAQQAASAI EAESKKAQVGPAPSAQSQVLDLSQYTRRAVSFLARNFNLYKVALVL 4666  
Db 4621 MEAQAAQQAASAI EAESKKAQVGPAPSAQSQVLDLSQYTRRAVSFLARNFNLYKVALVL 4680  
Qy 4667 AFCINFVLLFYKYSTLDGEGGSGGLDIIAGGSGGAGSGSGGSGGSGGSGGSGGSGGSGG 4726  
Db 4681 AFCINFVLLFYKYSTLDGEGGSGGLDIIAGGSGGAGSGSGGSGGSGGSGGSGGSGGSGG 4740  
Qy 4727 HIDEFFFYMEHVIMAAVHLHSIVSLAILIYYHLKVPILAIFKREKEIARKLEFDGLYIAE 4786  
Db 4741 HIDEFFFYMEHVIMAAVHLHSIVSLAILIYYHLKVPILAIFKREKEIARKLEFDGLYIAE 4800

Qy 4787 QPEDDDDLKSHWDKLVISAKSFPVNYWDKFVKKVKRAKYSYTDYDFDSISNMLGMEKTSFSA 4846  
Db 4801 QPEDDDDLKSHWDKLVISAKSFPVNYWDKFVKKVKRAKYSYTDYDFDSISNMLGMEKTSFSA 4860  
Qy 4847 QEBEGSKGLIHYIINIDRWYQVWKAGVTITDNSFLYSLWYFSFVSMGNFNFFFAAHLDD 4906  
Db 4861 QEBEGSKGLIHYIINIDRWYQVWKAGVTITDNSFLYSLWYFSFVSMGNFNFFFAAHLDD 4920  
Qy 4907 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIUVIYTVIAFNPERKFFVQOEDEDEVNRNC 4966  
Db 4921 VAVGFKTLRTILQSVTHNGKQLVLTVMLLTIIUVIYTVIAFNPERKFFVQOEDEDEVNRNC 4980  
Qy 4967 HDMLTCFVFNLYKGVKAGGIGDELBPPDGDSEVVRIFDIISFFFFIIIVILLAILQGLI 5026  
Db 4981 HDMLTCFVFNLYKGVKAGGIGDELBPPDGDSEVVRIFDIISFFFFIIIVILLAILQGLI 5040  
Qy 5027 IDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHPGFDTHVQREHNLANYNMFFLMHLI 5086  
Db 5041 IDAFGELRDQLESVKEDMESNCFICGINKDYFDKVPHPGFDTHVQREHNLANYNMFFLMHLI 5100  
Qy 5087 NKPDTEYTGQETTVNNMYTORCWDFFPVGDCFRKQVEDLAGE 5128  
Db 5101 NKPDTEYTGQETTVNNMYTORCWDFFPVGDCFRKQVEDLAGE 5142

RESULT 6  
US-10-668-767-8  
; Sequence 8, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCES: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 5127  
; TYPE: PRT  
; ORGANISM: Peregrinus maidis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (416)..(416)  
; OTHER INFORMATION: Xaa = Ile  
US-10-668-767-8

Query Match 80.7%; Score 21630; DB 4; Length 5127;  
Best Local Similarity 80.3%; Pred. No. 0;  
Matches 4174; Conservative 396; Mismatches 484; Indels 142; Gaps 46;  
Qy 1 MAEAGGASQDDVSEFLRTEDMVCLSCTATGERVCLAAEGFGRHCFLENIAADKNIPDDL 60  
Db 1 MADSEGG-SEQDDVSEFLRTEDMVCLSCTATGERVCLAAEGFGRHCFLENIAADKNIPDDL 59  
Qy 61 SQCVFVIEQALSVRALQELVTAAGSEGTGCTGSGHRTLLYCNAILLRHLNSDMYLACLST 120  
Db 60 STCVFVIEQALSVRALQELVTAAGSEGTGCTGSGHRTLLYCNAILLRHLNSDMYLACSST 119  
Qy 121 SSSODKLAFDVGLOQHSQSGACWMTLHPASKQSEGEKVRGDDLLIVSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVGLQEHSGQACWMTVHPASKQSEGEKVRGDDLLIVSVATERYLHTTK 179



Db 2309 HEMWACCRFLCVCRTSRQKAMFHPAFLLENSNILLSRSLRGSTFLDVAYSIME 2368  
Qy 2372 NTELALALRHYLEKIAVYLSRCLQSNLSBELVEKGYPDLGWDVPEGERYLDLFLRCVWVN 2431  
Db 2369 NTELALALRHYLEKIAIYLSRCLQSNLSBELVEKGYPDLGWDVPEGERYLDLFLRCVWVN 2428  
Qy 2432 GESVEENANLIVIRLLIRPECLGALRGEGLLKAIVDANKMSERTADRRKLREMOEG 2491  
Db 2429 GESVEENANLIVIRLLIRPPCLGALRGEGLLRAIVDANKMSERTADRRKVMDE-EPEG 2487  
Qy 2492 D---VNFSPHLPESDEDEDYDTGAATLNFCTLVLDLLRCAPDAGVIALGKQESLRARA 2548  
Db 2488 TTVMWHFEHPUPESDDEDDYDTGAAI LAFCTLVLDLLRCAPDSSVIAQKQESLRARA 2547  
Qy 2549 ILRSLVPLEDLOQVLSLRFTLNNPAAGEERPKSDMPGSLIPGHKQSVVLFLERVYGIETQ 2608  
Db 2548 ILRSLVPLEDLOQVLSLKFTLQNPAAAGEERPKSDMPGSLIPGHKQSVVLFLERVYGIETQ 2607  
Qy 2609 ELFYKLEBEAFLPDLRAATMLDRNDGCESDMALSMRYIIGNSILPLLIKHAYFNEAENY 2668  
Db 2608 ELFPRLLEAFLPDLRAATMLDRNDGSESDMALAMNRYIIGNSILPLLIHSHKFYNEADNY 2667  
Qy 2669 ASLLDATLHTVYRLSKNRMILTKGOREAVSDFLVALTSAMOPSMILKLLRKLTVDVSKLSE 2728  
Db 2668 ASLLDATLHTVYRLSKNRMILTKGOREAVSDFLVALTSMPQSMMLKULRKLTVDVSKLSE 2727  
Qy 2729 YTTVALRLTLHYERCARYGSTGAGQAGFASDEEKRLTMMLFNSIFDSLSKMDYEPE 2788  
Db 2728 YTTVALRLTLHYDRCARYGSTG-GOGLYGSSSDEEKRLTMMLFNSIFDSLSKMDYDPE 2786  
Qy 2789 LFGKALPCLIAIGCALPPDYSLSKNYDDEFYV-KEQAAGLDLNDPQDPOPIINTSSVALNN 2847  
Db 2787 LFGKALPCLIAIGCALPPDYSLSKNYDDELYGARDSQAGPSDGP-YNPQPIINTSHSVVLNN 2845  
Qy 2848 DLNTIVQFSHYHDWASRKIENGWYVGEWSDSQKTHPRLKPYNNLNDY----BKER 2902  
Db 2846 DLNTIVQFSHYHDWASRKIENGWYVGDQMSQKTHPRLKPYNNLNDYVPEISIERER 2905  
Qy 2903 YKEPVRESLKALLAIGMSVEHSEVDIPSNRSMRRQSKSGRPEIPEITDPSATPFDYNPH 2962  
Db 2906 YKEPVRESIKALLAIGWTVHESEADVPLTSGRSIRRSQK-----PNAWVDSSTFFNHPN 2960  
Qy 2963 PVDMTNLTLSREMOMNAERLAADNAHDIAWKKKKEELVTNGGGIHPQLVPYDILLTDKSKKK 3022  
Db 2961 PIDMTNLTLSREMOMNAERLAENAHDIWAKKKKEELITCGGIIHPQLVPYDILLTDKSKKK 3020  
Qy 3023 DRERSQBELKYLQYQGYKLRHPSK-APQSDTEQTTTGVATLREPAYSLLEKLIQYIDRAT 3081  
Db 3021 DRERSQBELKYLQYQGYKLRHPSRTGPFSESEQLAAQATGELREPAYSLLEKLIQYIDRAS 3080  
Qy 3082 INMKLLKPSTFFRRSSPKSTROIKPFKSAVLPLMEKYFSTHRNYFIATATANNVGA 3141  
Db 3081 INMKLLKPSTFFRRSSPKCTROIKPFKSVVLPLVEKYFSTHRNYFIATATANNIGAA 3140  
Qy 3142 SLKEKEMVAALFCKLASLLRSLRAAFGPDVIRIVRCLQVLVKIGDAKSLVKNCPEFIRTS 3201  
Db 3141 SLKEKEMVASLFCKANLLRSLRAAFGADVIRISVKCLQVLVKIGDAKSLVKNCPEFIRTS 3200  
Qy 3202 MLTFENNVADDVGHITIMNLQDKYAHLRGTHLKTSTSLGYINGVLLPLTLTAKFDHLANCE 3261  
Db 3201 MLTFENNTADDLGHITQNLQEGKYSHLRGAHLKTSTSLFYINDVILPVLTAAMPDHLAACE 3260  
Qy 3262 YGADLLDEIOVASVXMLGSLYALGTDAALTHDRKLYLKTETIERHKPALGSCIGAFSSTFP 3321  
Db 3261 YGSDLVLEIOVASVXMLGSLYITIGIDVLTLDHDKLYLKTETIDRHRPQLGRCLGAYASTFP 3320  
Qy 3322 VAFLEPHLNKQNSLNRRIADHLSLEAQDINQKMEQCMTLETILGEVDQFVESDKTYNE 3381  
Db 3321 VAFLEPHLNKQNSLVNRIADHLSLEAQDILSRMESTMPTLDNLILSEVDQFVESDKTHND 3380  
Qy 3382 APHIDVVLPLLCYLPFWAQGDNDVPTCGNHVMTVTAENHQLLKNVLLKIKKNIGN 3441

Db 3381 APHIDVIMPLCSYLPVWMOQPDNVALTAGNVVTTVTISEHMQNQLLKNVLLKIKKNIGN 3440  
Qy 3442 ENAPWMTTRATYTOOIIINSSEELLRSDSFLPLAERYKRTDNNPHKEESLRGFTKSSTDD 3501  
Db 3441 ESAPWMTTRIAAYTOOIIINSSEELLKDDPFLPLAERYVKKRTDAMPHKEESLRGFTKSASDD 3500  
Qy 3502 TSQVESQIOEDWOLLVRDIYSFYPLLIKYVDLQRNHLNRNNVPEABEYLNVHVAIEFINWS 3561  
Db 3501 TSQIEAQIOEDWOLLVRDIYSFYPLLIKYVDLQRNHLNRNNISEAEDLYNHVAIEFINWS 3560  
Qy 3562 KSOYFLKEBQNFISANEIDNMVIMPTATRRVAVTDGT--POGGGKKKKKKHDKKDKD 3619  
Db 3561 KSOYFLKEBQNFISANEIDNMVIMPTATRRSAVSDSAAPPGSGSGKKKKKRNREKKDKD 3620  
Qy 3620 KEVQASLMVACLKRLLPVGLNLPAGREQLVOHCKORFLKMKSEQDVAEFAKTQTLTLPDK 3679  
Db 3621 KELQASLMVACLKRLLPVGLNLPAGREQLVOHCKORFLKMKQDYEIFEFAKTQTLTLPDK 3680  
Qy 3680 IDPADMSWQHYLYSKLGSKSKSNITVETAENKAKIIDTVERIVAMSKVLFGLHMTDHP 3739  
Db 3681 LDPEDEMSWQHYLYSTLGSKKEI-----TEGGKPEQIDAVVDRIVAMAKVLFGLHMTDHP 3735  
Qy 3740 QOMSKNVIYSVVSIOKRRAVIACFRQTSLSHSLPRHACNFARTYIELWELBEENIGQVVM 3799  
Db 3736 QLQSKASYRSVVSTQKRAVIACFRQLSLHALPRKAINIFARSYFVYELWELTEENVGTEVL 3795  
Qy 3800 IEDLTQSFEDEALKKSD-VVEEGEKDPLTQIYVTTFCRGANTERSGALQBDPLVMSYAH 3858  
Db 3796 IEDLTQSFEDEALKKSDDEYDEG-KSDPLTQIYVTTFCRGANTERSGALQBDPLVMSYAEI 3854  
Qy 3859 IAKSCGEEBEGGEEBEGGEEAEDEBGRASIHQEMEKQKLLFHOARLADRGVABMVL 3918  
Db 3855 AAKSCGEEBEGGEEBEGGEE--EGBEQG-ASHQEMEKQKLLFHOARLANRGVABMVL 3909  
Qy 3919 LHISASKGLPSENMVMTLQIGISILRGGNIDIQMGMLNHLKOKKQVGFSTSIAGLMNSCS 3978  
Db 3910 LHISACNVPSDMVEKTLQIGISILRGGNIDIQMGMLNHLKOKKQVGFSTSIAGLMNSCS 3969  
Qy 3979 VLDDAFERNTKAEGLVGLEGAGEKNMDAFTCALFRFIQLTCTCGHNLDMQNYLRQ 4038  
Db 3970 VLDDAFERNTKAEGLVGSDGAGEKNMDAFTCTLFRFIQLTCTCGHNLDMQNYLRQ 4029  
Qy 4039 AGNTTNNVVICVVDYLLRQESIMDFYHYSKELIDPAGKANFFKAI GVASQVFNLT 4098  
Db 4030 AGNTTNNVVICVVDYLLRQESIMDFYHYSKELIDPAGKANFFKAI GVASQVFNLT 4089  
Qy 4099 EVIQGCTQNOQALAHSLMDAVGGFLFLFSHMQDKLSKISSQVDLLKELLNLQKMDIPM 4158  
Db 4090 EVIQGCTQNOQALAHSLMDAVGGFLFLFSHMQDKLSKISSQVDLLKELLNLQKMDITM 4149  
Qy 4159 MLSMLEGNVNGTIGKQWDTLVESASNVLEILKYFDMFLKLDLTSSASFQETDANNDG 4218  
Db 4150 MLSMLEGNVNGTIGKQWDTLVESASNVLEILKYFDMFLKLDMTAPSFLEIDPNHGD 4209  
Qy 4219 WVLKDPFKEMEQKSYTPEIEBFLACCTNHDGKLDYIGFCDRFHEPAKEIGFNLAVL 4278  
Db 4210 WVLKDPFKEMEQKSYTTEEISFMLQCCCTNHDGKVDYIGFVDRFHEPSKEIGFNLAVL 4269  
Qy 4279 LTNLSEHMPNEPLARFETAGSVLNFEPFLGRIEIMGSKRIERYFEI KESNIEQWE 4338  
Db 4270 LTNLSEHMPNEPLARFETAGSVLNFEPFLGRIEIMGSKRIERYFEI KESNIEQWE 4329  
Qy 4339 KPQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHASGLMAASEESVGTKNRE 4398  
Db 4330 KPQIKESKRAFFYSIVTEGGDKLEAFVNFCEDAIFEMTHASGLMSVDDDSGGG--GGK 4387  
Qy 4399 ASYVMGDDDDERAGKDPERRQSVKQGVATAPSSLSPSNIAKIAMQOOMPAAELAVG 4458  
Db 4388 AAYTISEDEEKNAPDIRTTOAFKDAIYFILTMLSPSNIKTKINEMQOMSVPVELVVG 4447  
Qy 4459 FFKMFFYLYVYGVLLVVVRYIFGVLLGLMRGQTDPEPPPEEPEEKI-GOLRHRLLAT 4517  
Db 4448 FFKIFFYFYSGFSVSVLRYFGRILMTLMRGQTEEPVAEVKKEDEIMGPI-----4500

Qy	4518	QSSRHLPPALPPADDTGQMVSASFGLDITTKEDNGOIQVKPHESPST-STPSSGEE-----4570
Db	4501	--RALP--PPPDNKEASSSS-----AKODSG--QAKPADGGATLALTASGEHEKGGA4548
Qy	4571	-----AEVSPDESADTHEEQPPSLIDLLGGEQAKQKQOERMEQAQAQAAMSAIAEASKK4626
Db	4549	TEBGAEDGAKPEGAETTEGTTMTLADLLGGEAAKKEAVASAEVAEQQAQMAVAEAEAKH4608
Qy	4627	AVQGPAPSALSOVDLSQYOTRRASFLARNFYNLKYVALVLAFCINFVLLFYKYSTL-----4682
Db	4609	EVVS--EPSASQIDFNRYTHRASFLARNFYNLKYVALVLAFCINFILLFYKVTYLGED4667
Qy	4683	-DGEGBE-GSGLGDII---AGGGSG--SGAGSGDGSGESGED-----DDALEVHVHID4731
Db	4668	DDGSGSELGGLAEADLLEELGGSGEBGGGLSGISGESGEDSGSEEDPIELHVHVED4727
Qy	4732	FFYMEHVIKAAVNLHSIVSLAAILGYIHLKVPLAIPKREKIEARKLEFDGLGYTAEQPEDD4791
Db	4728	FFYMAHVMIKAAMLHSIVSLAMLIAYIYHLKVPLAIPKREKIEARRLEFDGLGYTAEQPEDD4787
Qy	4792	DLKSHWDKLVISAKSPFVNVWDFVKVKKVAKYSETYDFDISINMLGWEKTSFSAQBEEG4851
Db	4788	DIKSHWDKLVISAKSPFVNVWDFVKVKKVQKQYSETYDFDISITLLGWEKTSFSSQTEE4847
Qy	4852	SKGLIHYIINIDRWYQWKAGVTTITDNSFLYSIMWYFSFGMGNFNNFFFAAHLLDVAVGF4911
Db	4848	GTGIINFILNIDRWYQWKAGVTTIDNAFYLSLWYFISILGNFNNFFFAAHLLDVAVGF4907
Qy	4912	KTLRTILQSVDTHNGKQLVLTVMLLTIIYIYTVIAFNPFKRYVQOESDDEVNRRNCHDMLT4971
Db	4908	KTLRTILQSVDTHNGKQLVLTVMLLTIIYIYTVIAFNPFKRYVQOESDEEDVKKCHDMLT4967
Qy	4972	CFVFNLYKGVRAAGGIGDELEPPDGDSEVYRIIFDISFSEFFIIVILLAIQGLIIDAFG5031
Db	4968	CFVFNLYKGVRAAGGIGDELEPPDGDSEVYRIIMFDITFFFFVIVILLAIQGLIIDAFG5027
Qy	5032	ELRDQLESVKEDMESNCFICGINKDYFDKVPHGFDTHVQREHNLANTYMFFLMHLINKPDT5091
Db	5028	ELRDQLESVKEDMESNCFICGIGKDYFDKVPHGFDTHVQOEHNLANTYMFFLMHLINKPDT5087
Qy	5092	EYTGQETVYVMNYTORCWDFPFPGDCFRKQVEDLMG5127
Db	5088	EYTGQETVYVMNYOORCWDFPFPGDCFRKQVEDELG5123

[illegible]



Db 960 IFMOGNGYKPAPLDLISA VTLTKPLEELVDQLAENTHNLWARERIQOGWTYGLNBSNHR 1019  
Qy 1021 SPHLVPYKVDADAIKKANRDASTVTRTLVYGYMLDPPGTEOHEALLLEASKQKQADR 1080  
Db 1020 SPHLVPYAKVDEAIKKANRDASTVTRTLVYGYVLDPPPTGEGTEALLAQAURLKFAGR 1079  
Qy 1081 TYRAEKYAVSSGKWYFEFELTAGPMRVGWAHADMAPGMMLOGDENSWAFDGYNEEKVY 1140  
Db 1080 TYRVERNAYVTSWKYFEFEVLTSOPMRVGHARADCVPGMGLSGEDTSWAFDGHNEEKVY 1139  
Qy 1141 SGNTESEKQWAVGVGVFLDLIDKITSISLINGELLMDALGGTTTADV--QGDNFVPA 1198  
Db 1140 GGVSSEFGKQCGDVGFLDLADHTISFSLINGELLMDALGGTTTADVTAEGVFVPA 1199  
Qy 1199 CTLGVGKARLYQGVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWTKOPIFENTDEM 1258  
Db 1200 CTLGVGKARLYQGVNTLKYFTTCGLQEGYEPFCVNMRRPVTHWTKOPIFENTDEM 1259  
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTPETMEKANWFLRLSLPVIChNEPTIDEAEKARRW 1318  
Db 1260 PDCRIDVTRIPGGADTPPHLKISHNTPETMEKANWFLRLSLPVTGCEPISBQEKARRW 1319  
Qy 1319 VEIKDRQOILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371  
Db 1320 DEIKNRQYRLMREAIEIAAQMVQVQAAHMDHMLKGGFNNDIKGLTRNFDHADAEADHM 1379  
Qy 1372 KRLSPRPKCSMTRGVTIQNNYLQGVNGMHRSTSEAMAKYDLAGOGLTPDDKKDK 1431  
Db 1380 MRGNRPKSGSLRNIT---FETDMSAALDEMQRSTS-----VLDNMGLGEEMDDKK-K 1430  
Qy 1432 RGRSPKFFRSKRGESSDRAKSRKTPDPSPDTEVSPGERGARRPNQIKVSQANQRYNG 1491  
Db 1431 RGRSPKFFR-SKSRDQGREK-MGARLTDTSLERRNTVAGHRNVNVNQMTTRAPTLRLNN 1488  
Qy 1492 MNARPSRNLXGSOVGLNMAFTQDRKQMTTSTLQAASATETVGNIEFDAECLKLINEFY 1551  
Db 1489 AEIppspv-----PQPKQLSGSNLQGPVETSGDMEFDAECLKLINEFY 1534  
Qy 1552 GVRYPGQDPHVYIGWTTQYHLHSDKDFNQSRYTKSGSVITDDYDRVENNVNRQSCYMV 1611  
Db 1535 GVRIFPGQDPHVYIGWTTQYHLHSREFNKNVRRGSVYIEDDYEMAIERIDRQSCYV 1594  
Qy 1612 RADELXNEVMAEATAKAGSQGMFTGCSVDSTGTSVSFTCEGKDTSGFKPMPEPKLPAPAI 1671  
Db 1595 RADELNEVTDQAGKAGSQGMFCGFVDATGIRFTCEGKDTSHRMMEPDTKLPAPAI 1654  
Qy 1672 FVEATSEKILQIELGRSATSPLSAAVLPTSDKHVIFQFPPLRKVQCLKPHQWARVPNQS 1731  
Db 1655 FVEATSEKILQIELGRPTTTLPLSAAVLPTSDKHINPQSPPLRKVQCLRPHQWARVPNTA 1714  
Qy 1732 LQVHALKLSIDRGWSMLCEDAVSMLALHIPEDRCIDILEPIEMDKLLSPHSHTLTLYAA 1791  
Db 1715 LQVHALKLSIDVRGWSMLCEDVPVSMALHIPEDRCIDILELIENDKLLSPHSAHSLTLYAA 1774  
Qy 1792 LCYOSNRAAALCTHVDOKOLLVAISOYVNSGPLRGQFYDLLLALHSHATTMEACKN 1851  
Db 1775 LCYOSNRAAALCOHVQKOLLVAIRSEYNSGPLRGQFYDLLLALHSHATTMEACKN 1834  
Qy 1852 EFVPLPGLPELKALYEEPMDGMSLSLQTESVRPQMKMTDI-----AESITE 1897  
Db 1835 EYITPLGNELKELYSDEEMQHSLSASLVTESVRPQLRMTETITPPVIATSSMPSVSSEPIPD 1894  
Qy 1898 ISNLYSPYFPLEVAREFVQALABAVETNQVHNRPDVPVGSNENIPLPLIKVLDRLLLVGM 1957  
Db 1895 IDQLYSPKFFLEVVRQFVMEALKDAVEINQVHNRPDPIGWTNENIPLPLIKVLDRLLLVG 1954  
Qy 1958 MRDEDVEKLLTWTNPETWDPDFDEKGDHFKGLLHMKWAGKALQWCYLLQHLNDQLR 2017  
Db 1955 LTDEBQRLLVNIDPETWDQAFEREGKDEHFKGLLTKWQAGKALQWCYLLUHLUDYDQLR 2014  
Qy 2018 HRVEAIIAFADHFDVGDQLDQLRYTEIKQSDPLPSAAAKKTRBFCPPRQMNAILSPK 2077  
Db 2015 HRVESIIAFSHDFVGDQLDQLRYTEIKQSDPLPSAAAKKTRBFCPPRQMNAILCFK 2074

Qy 2078 HLEEDKENCPCGEEIARMNEPHDTLMAHVSLSHALQEPDAAENQOE-PEAKPGAFGKLYN 2136  
Db 2075 NLEPDQDNCTCGLRGLRGDLDFHDSLMQKVSLSNALQEPDGVGTALEEYVKTPITKIYN 2134  
Qy 2137 IINTVKELEBEAKAIEBPPKKTPEEKFRKVLITOTIVNVAESQIETPKLVREMFSLVRQ 2196  
Db 2135 FINTVKELEBGPKEVEPEKKTPEEVFRKVLIKTIVSWAESQIENPKLVREMFSLLRQ 2194  
Qy 2197 YDAGELIRALEKTYVINAKTKLDVAMVMVGLSOIRALLPVQMSOEBEELMRKELWLVN 2256  
Db 2195 YDTVGLSRALEKTYVINTRARDVAMVMVGLSOIRALLPVQMSOEBEELMRKELWLVN 2254  
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMNTLGRRAQAQSDAOPSSQPVAB--DSKEKDTSHEM 2314  
Db 2255 NATFFQHPDLIRVLRVHENVMAVMNTLGRRAQAQSDA-PTQSEVAEGASKEKDTSHEM 2313  
Qy 2315 VVACCRFLCYFCRTGRQNKAMFDFHFDLLENSNILLSRPLSGSTPLDVAYSLSMMENTE 2374  
Db 2314 VVACCRFLCYFCRTGRQNKAMFDFHFDLLENSNILLSRPLSGSTPLDVAYSLSMMENTE 2373  
Qy 2375 LALALREHYLEKIAVLSRCGLQSNSELVEKGYPDLDGWDPEGERYLDLDFRCVWNGES 2434  
Db 2374 LALALREHYLEKIAVLSRCGLQSNSELVEKGYPDLDGWDPEGERYLDLDFRCVWNGES 2433  
Qy 2435 VEENANLVIRLLIRRRPECLGPALRGEGGLLKAIVDANKMSERIAADRRKLREMEQEGDV- 2493  
Db 2434 VEENANLVIRLLIRRRPECLGPALRGEGGLFRAIVEANRMSERISDRCKMWD-EAEGTIA 2492  
Qy 2494 --NFSHPLPESDDEYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESIRARAILR 2551  
Db 2493 GLNFTHPLPEGEDEYIDTGAAILNFYCTLVDLLGRCAPDASVIEQKNESIRARAILR 2552  
Qy 2552 SLVPLBDLQGLVLSRLTLANPAAGEBERPKSDMPSGLIPGHKQSVGLFLEBYVIGETQLF 2611  
Db 2553 SLVPLBDLQGLVLSKFTLSQTAPGEBKPKSDMPSGLIPNNKQSVLFLFLEBYVIGEAQDLF 2612  
Qy 2612 YKLEBAFIPDLRAAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNAENYASL 2671  
Db 2613 YRLLEDAFIPDLTATILDKSOGSDMALAMNRYIGNSILPLLIKHASKFYNAENYASL 2672  
Qy 2672 LDATLHTVYRLSKNRMILTKQREAVSDFLVALTSQMAPAMLLKLLRKLTVDVSKLSBYTT 2731  
Db 2673 LDATLHTVYRLSKNRMILTKQREAVSDFLVALTSQMAPAMLLKLLRKLTVDVSKLSBYTT 2732  
Qy 2732 VALRLLTLHYERCAKYGTGACQAGAFGASSDDEKRLTMMLFSNI PDSLSKMDYEPLEFG 2791  
Db 2733 VALRLLTLHPDRCAKYGST-QQGSYGASSDDEKRLTMMLFSNI PDSLSNMDYDPELFG 2791  
Qy 2792 KALPCLIAIGCALPPDYSLSKNYDDBFYGKEQAAGDLDPQYDPOPIINTSSVALNNDLNT 2851  
Db 2792 KALPCLIAIGCALPPDYSLSKNTDEYDYGROMCAP--DQOYMPNPDTNNVHLDNDLNS 2849  
Qy 2852 IVQKFSHYHDAWASRKIENGWYVYGEWSDSQKTHPRKLPYNMLNDYKEKRYEPVRESL 2911  
Db 2850 LVQKFSHYHDAWASRLGEGWTYDIRSDNDRKHPRLKFPYNMLSEYERERYRDPVRECL 2909  
Qy 2912 KALLATGWSVEHSEVDIPSNRSMRQSKSGRPEI--VTDSATPFDPNPHVDMTNL 2969  
Db 2910 KGLLAIGWTVEHSEVEVALNHRGSTRQSK-----PQINEFQNEGSPFNPHVDMNSNL 2964  
Qy 2970 TLSREMNMAERLADNAHDIIWAKKKEELVTNGGHPQVYDILLTKKKKDRERSQE 3029  
Db 2965 TLSREMNMAERLAEASHDIWAKKKEELNGCGVHPQVYDILLTKKKKDRERSQE 3024  
Qy 3030 FLKYLOYQGYKLRHPSKAPQSDTEQTTTGVVAIELRFAYSLSLEKLIQYIDRATINMKLLKP 3089  
Db 3025 FLKYMQYQGYKLRHPSKGGAVE--EGGATQAAVELRFSYSLEKLIQYIDRATINMKLLKP 3083  
Qy 3090 STTFSRRSSPKTROIKFFSKAVLPLMEKYFSTHRNYFIAVATATNNVGAASIKEMV 3149  
Db 3084 STTFSRRSSPKTATROIKFFSKVVLPLMEKYFSTHRNYFIAVATATNNI GAASIKEMV 3143





APPLICANT: Smith, Rejane  
APPLICANT: Tao, Yong  
APPLICANT: Wu, Lihong  
TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
FILE REFERENCE: BBI533 US NA  
CURRENT APPLICATION NUMBER: US/10/668,767  
CURRENT FILING DATE: 2003-09-23  
PRIOR APPLICATION NUMBER: 60/412,795  
PRIOR FILING DATE: 2002-09-23  
PRIOR APPLICATION NUMBER: 60/427,324  
PRIOR FILING DATE: 2002-11-18  
NUMBER OF SEQ ID NOS: 149  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 121  
LENGTH: 5113  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: gi 17352467  
US-10-668-767-121

Query Match 79.8%; Score 21376; DB 4; Length 5113;  
Best Local Similarity 79.1%; Pred. No. 0;  
Matches 4090; Conservative 447; Mismatches 523; Indels 108; Gaps 40;

Qy 1 MAEAGGASODDVSFURTEDMVCLSTCTATGERVCLAAEGFGRNRCFLENIAADKXIPDDL 60  
Db 1 MAEAGG-SEQDDVSFLRTEDMVLSTCTATGERVCLAAEGFGRNRCFLENIAADKXVPPDL 59  
Qy 61 SOCVFVTEALSVRALQELVTAAGSETCKGSGHRLLVGNATLLRHNSDMYLACLSL 120  
Db 60 SOCVFVTEALSVRALQELVTAAGSETCKGSGHRLLVGNATLLRHNSDMYLACLSL 119  
Qy 121 SSSQDLAFDVLQOHSQGEACWTLHPASQORSEGEKVRVGGDLILVSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVLQOHSQGEACWTLHPASQORSEGEKVRVGGDLILVSVATERYLHTTK 179  
Qy 181 ENEVSIVNASPHVTHWSVQYGTGIRSMKYGVYVFGDVLFPFHGGDECLTIPSTWYKDG 240  
Db 180 ENEQSIVNASPHVTHWSVQYGTGIRSMKYGVYVFGDVLFPFHGGDECLTIPSTWGRE 239  
Qy 241 GQNTVVYEGGSMQASRLWELARTKWKAGCFINWHPMRIHTTGRYLGVNDQNELY 300  
Db 240 GQNTIVYEGGVMAQASRLWELARTKWKCGFINWHPMRIHTTGRYLGVNDQNELI 299  
Qy 301 LVSRREATAFACLRQEKDDQVLEKDXLEVIGAPIIKYGDSTVIVQHSSETGLWLSY 360  
Db 300 LVKKEASIAITTCLEQEKDEKKVLEKDXLEVIGSPIIKYGDTTVIVQHCETSLWSY 359  
Qy 361 KSYETKKGVGVBEKQAILHEBGMDGLDFSRSQBEESRTARVIRKCSLSLFTKINGL 420  
Db 360 KSYETKKGVGVBEKQAILHEEGKMDCLDFSRSQBEESRTARVIRKCSLSLFTQFITAL 419  
Qy 421 ETLQENRHSFASVNLGEMVMCLDLINYPADQDEMEHEBKONKFRALRNQDLFOE 480  
Db 420 ETLQSNRRHSIFFOKNVNLNEMVMCLDLINYPQEDDMEHEBKONKFRALRNQDLFOE 479  
Qy 481 EGIILNLEADKINVTISQGLAGDSGQSWEMISGYLQLLAAIIGKNTNCAQ 540  
Db 480 EGVNLNLEADKINITSQGLASFLAGDGTGSWDLISYLYLQLLAAIIGKNTNCAQ 539  
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMVLVHCVLIDSPALNMNRDEHIKVIISLLEKHGR 600  
Db 540 FANSNRLNWLFSRLGSQASGEGTGMVLVHCVLIDSPALNMNRDEHIKVIISLLEKHGR 599  
Qy 601 DPKVLDVLCISLVGNGVAVRSQNNICDYLPGKNLLQTLVLDHVSVRNIEFVGRVGE 660  
Db 600 DPKVLDVLCISLVGNGVAVRSQNNICDYLPGKNLLQTLVLDHVSIRNIEFVGRVGE 659  
Qy 661 SAVRYKWFYFVTMDHIEQTTHMPLHRIGWANTTGYVPYPGGKGWGGVGDLLYSYGF 720  
Db 660 SSMYQKWFYFVTMDHIEQTTHMPLHRIGWANTTGYVPYPGGKGWGGVGDLLYSFGF 719

Qy 721 DGAYLWSGGRKTPVNRTHAEPEYIRKGDVIGCALDLTVPIINEMENGVRVTGSGTFNENLE 780  
Db 720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITTFNCGVKVGRGFRDNLD 779  
Qy 781 GMEFFPVISCSSKLSRFLGGEHGRLYRAAPEGYSPLVESLLPQOILSLSPCFYFGLSK 840  
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Qy 841 RALAGPPLVODDTAFVPTPVDTLQITLPTVYEQIRDKLAENIHEMMANMKIEAGWYGDQ 900  
Db 840 NVLAGPWLIEDDTAFVPPKPVDTTGTLPSSVDQIKELAEINHEMMALNKIEAGWSGEH 899  
Qy 901 REDLHKHPCLVPFERLPAAEKRYDQLAVQTLTKTILALGYISLDKPPARIINRVLNPE 960  
Db 900 RDDYHRIHPCLTHPEKLPAAEKRYDQLAVQTLTKTISLGYYITMDKPPARIINRVLNPE 959  
Qy 961 PFMQSNQYKPAPLDLSAVTLTPKMDLBDVLAENHNLWARERIQQGWTYGLNEDSDMR 1020  
Db 960 IFMQNGYKPAPLDLSAVTLTPKLEBELVLAENHNLWARERIQQGWTYGLNEDSENHR 1019  
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Qy 1081 TYBAEKYAVSSCKWYFEPEILTAGPMRVGMHADMAPGMMLGQDENSNAFADGVNEBKVY 1140  
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Qy 1141 SGNTEFGKQWAGVDVGVVFLDLIDKTSIFSLNGELMLDALGETTTPADV--QGDNFVPA 1198  
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Qy 1199 CTLGVGQKARLTQGVQDNTLYKFTTCLQEGYPPPCVMKRDVTHWTKQOPIFENDEM 1258  
Db 1200 CTLGVGQKARLTQGVQDNTLYKFTTCLQEGYPPPCVMKRDVTHWTKQOPIFENDEM 1259  
Qy 1259 IDTRIDVTRIPAGSDTPCLKISHNTFETMEKANWFLRLSLPVICHNEFIDAEKARRW 1318  
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Qy 1319 VEIKDRQOILMKEA-VEAQW-----PAHIDQIMRSGFTMNDIKGLHYE-DNQBELPSSKM 1371  
Db 1320 DEIKNRQYRLMREAEIAAQOVQTAHMDHMLKGGFNMDIKGLTRNFDHADAADHM 1379  
Qy 1372 KRUPSPPRKGSTVRGVTIONYNLQPGVQNGHMRSTSEAMAKYDLGAQGLTDDDKDK 1431  
Db 1380 MRGNPFRKSGSLTRNIT---FETDMSAALDEMQRSTS-----VLDNMGLGEEMDDKK-K 1430  
Qy 1432 RGRSPKFRSKGESSDRASRKSPTDPSDTEVSPERGARRPNPQIKVSOANORYNG 1491  
Db 1431 RGRSPKFRSKGESSDRASRKSPTDPSDTEVSPERGARRPNPQIKVSOANORYNG 1488  
Qy 1492 MNARSPRTNLGYSQVGLNMAATPQDRKQMTTSTAQSATETVQNEIPDAECLKLINIFY 1551  
Db 1489 AEIPSPV-----PQPKQLSGSNLQGPVETSGDGMFDEAECLKLINIFY 1534  
Qy 1552 GVIYPCQDPDTHVYGVVTHYHLHSDFNQSKVTKSSVIIITDDYDRVAVENVRQSCVMY 1611  
Db 1535 GVIYPCQDPDTHVYGVVTHYHLHSDFNQSKVTKSSVIIITDDYDRVAVENVRQSCVMY 1594  
Qy 1612 RADELNEVMAEATAGASOGMFIQGVSDTSTGVSFTCSGKDTSPKFKMEPETKLPFAI 1671  
Db 1595 RADELNEVQDASGKASOGMFIQGVSDTSTGVSFTCSGKDTSPKFKMEPETKLPFAI 1654  
Qy 1672 FVEATSKELIQIELGRTPPTLPLSAVLPSTDHINPQSPPLKVKQCLRPHQWAVPNTA 1714  
Db 1655 FVEATSKELIQIELGRTPPTLPLSAVLPSTDHINPQSPPLKVKQCLRPHQWAVPNTA 1714  
Qy 1732 LQVHALKSLDIRGWSMLCEDAVSNLALHIEPDRCDIDILEPIMDKLLSHSHTLTLYAA 1791  
Db 1715 LQVHALKSLDIRGWSMLCEDAVSNLALHIEPDRCDIDILEPIMDKLLSHSHTLTLYAA 1774  
Qy 1792 LCYQSNVRAAHALCTHVDQKQLLYAISOYQWSGFLRQGFYDILLIALHLESHATTMEACKN 1851

Db	1775	LCVQSNRAAHALCQHVQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCN	1834	Db	2850	SRLEGQWYGDIFSDNDRKHPRILKPYNMLSEYERERYROPVRRECLGKLLAIGTWVEHSE	2909
Qy	1852	EVPIPLGELKALYEEPDGMSHLSRLOTESVRPQMKTMDIAESITENSLYSPYPLEVA	1911	Qy	2926	VDIPSNRRSNMRROSKSGGRPPEI--VTDSATPDYPNPHVDMTNLTLSREMOMNAERLA	2983
Db	1835	EYITPLGAELEKELYSDEENQHSRLSVTESVRPQURMTETIETIPIDIDOLYSKPPELV	1894	Db	2910	VEVALNHRGSTRROSK-----PQINEFQNEGSPENYNPHPVDMSNLTLSREMOMNAERLA	2964
Qy	1912	REFVMOALAEVETMQVHNRDPVGGSNENLFLPLKLDRLLLVGMWDEDEVEKLLIMTN	1971	Qy	2984	DNAHDIWAKKKBELVTNGGIIHPQVDPYDILLTTOKEKKKDBERSQEBFLKYLOYQYKLUHR	3043
Db	1895	RQFVMEALKDAEINQVHNRDPIGWTNENLFLPLKLDRLLLVGVLTDEDVQRLLVVID	1954	Db	2965	ENSHDIWAKKKNEELNGCGVHPQVDPYDILLTTOKEKKKDBERSQEBFLKYQYQYKLUHK	3024
Qy	1972	PETWPSFDEKGBEHRKGLLHKWABGAKLOCMYLLLOHLNDIQRHRVEAIIAPAHFV	2031	Qy	3044	PSKAPQSDTEQTTTGVATIELRFAYSLLLEKLIQYIDRATINMKLLKPSFTFSRRSSFKTST	3103
Db	1955	PETWQAFEREKGBEHRKGLLTKMAEGAKLOCMYLLLHLLHYDTQLRHRVESIIAFSHDFV	2014	Db	3025	PSKGAGVE--EGGATQAAVELRFSYLLLEKLIQYIDRATINMKLLKPSFTFSRRSSFKTAT	3083
Qy	2032	GLQOTDQRLRYTEIKOSDLPSSAVALKTEFPFCPREONNATLSFKHLEEDKENCPCGE	2091	Qy	3104	RDIKFFSKAVLPLMEKTFSTHRNYFIAVATATNNVNGAASLKEKEMVAALFCKLASLLRSR	3163
Db	2015	GLQOTDQRLRYTEIKOSDLPSSAVALKTEFPFCPREQNNQILCCFNLEPDODDQCTCGL	2074	Db	3084	RDIKFFSKVVLPLMEKTFSTHRNYFIAIATATNNGAASLKEKEMVASIFCKLAALLNR	3143
Qy	2092	ELIARMEFHDTLMAHVSJLHALQEPDAENQBE--PEAKPGAFGLKLYNIINTVKELEEEBAKA	2150	Qy	3164	LAAPGPDVRIIVRCLOVLVKGIDAKSLVQNCPEFIRTSMLTFFFNVADDVGHITMNLQDG	3223
Db	2075	ELRGRLGDFHDSLMQKVSJNALQEPDGVGTALIEVKTGPIITKIYNFINTVKELEBEGPKE	2134	Db	3144	LSAFGPDVRIIVRCLOVLVKGIDARTLTTKNCPFI RTSMLTFFFNQTSDDLGNLTILNLQDG	3203
Qy	2151	IEBPCKTPEEPRKRVLIQTIYVNAEESQIETPKLVREMFSLLVROYDAVGBELIRALEKT	2210	Qy	3224	KYAHLRGTHLKTSTSLGYINGVLLPILTAKEFDHLANCEYAGADLLLDEIQVASYKMLGSLY	3283
Db	2135	VEEPEKTPPEEPRKRVLIQTIYVNAEESQIENPKLVREMFSLLVROYDVTGELVRALEKT	2194	Db	3204	KYSHLRGTHLKTSTSLGYVNVQVLPVLTAMFDHLAACDYGSDLLLDEIQVASYKILAAY	3263
Qy	2211	YVINAKTKLDVAMVWGLSQIRALLPVMQSQEESBELMRKRLWKLYNNHTFFQHPDLIRVL	2270	Qy	3284	ALGTDASLTHDRKYLKTEIERHKDPALGCLGAFSTFPVAFLEPHLNKHQNFSLNRIAD	3343
Db	2195	YVINTRARDVAMVWGLSQIRALLPVMQSQEESBELMRKRLWKLYNNATFFQHPDLIRIL	2254	Db	3264	HLGTDGLTHDRKYLKTEIERHRPALGCLGAYSSCFVAFLEPHLNKHQNSULNRIAD	3323
Qy	2271	RVENHMAVMNTLGRRAQAQDAOPSSQPVAE--DSKEKDTSHEMVACCFVCFRT	2328	Qy	3344	HSLEAQDIMQKVEQCMPTLETILGEVDQFVESDKTYNEAPHI IDVVLPLLCYSYLPFWNAQ	3403
Db	2255	RVENHMAVMNTLGRRAQAQDA--PTQSEVAEGAPSKDKTSHEMVACCFVCFRT	2313	Db	3324	HSLEAQDIMVQVESCMPTLETILAEVDQFVESDKTYNDAPHI IDVILPLLCAYLPFWMSQ	3383
Qy	2329	GRQNKAMPDFHDFLLENSNILLRPSLRGSTPLDVAYSSLMENLTELALAREHYLEKIA	2388	Qy	3404	GPDNVTPGGNHVMTVAEHNNQLLKNVLKLI KKNIGNENAPMWTRIATYTOQIIINSSE	3463
Db	2314	GRQNKAMPDFHDFLLDNANILLRPSLRGSTPLDVAYSSLMENLTELALAREHYLEKIA	2373	Db	3384	GPDNVSPSGNHVMTVMTADHNNPLLRNVLMKI KKNIGNDNAPMWTRIATYTOQIIINSSE	3443
Qy	2389	VYLSRCGLQSNSELYKGVDPDGLGWDPVEGERVLDLFCVWVNGSVENANLVRILLIR	2448	Qy	3464	ELLRDSPLPLAERVKRTRDNMFHKEESLRGFIKSTDDTSQVESQIQBDWQLLVDRDIYSF	3523
Db	2374	VYLSRCGLQSNSELYKGVDPDGLGWDPVEGERVLDLFLRYCVWVNGSVENANLVRILLIR	2433	Db	3444	ELLKDPFLPLAERVKRTRDNMFHKEESLRGFIKSTDDTSQVESQIQBDWQLLVDRDIYSF	3503
Qy	2449	RPECLGPAIRGEGGLKAIIVANKMSERIDRRKLREMEQGDV--NFSPHPLSESD	2505	Qy	3524	YPLLIKYVDLQNRNHWLNVPPEABEELYNHVAEIFNINWSKQYFLKEEQNFISANEIDNNV	3583
Db	2434	RPECLGPAIRGEGGLKAIIVANKMSERIDRRKLREMEQGDV--NFSPHPLSESD	2492	Db	3504	YPLLIKYVDLQNRNHWLNVPPEABEELYNHVAEIFNINWSKQYFLKEEQNFISANEIDNNV	3563
Qy	2506	EYIDTGAAILNFYCTVLDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL	2565	Qy	3584	LIMPTATRRVAVTDGTPQGGG--KKKKKHDKKDKDKQVQASLMVACLKELLVPVGNL	3641
Db	2493	EYIDTGAAILNFYCTVLDLLGRCAPDASVIEQKNESLRARAILRSLVPLEDLQGVLSL	2552	Db	3564	LIMPTATRR--SAISEGAPAVGGKVKKKKKXNRDKKDKDKQVQASLMVACLKELLVPVGNL	3622
Qy	2566	RFTLNNPAAGBERPKSDMPGSLIPGHQKQVGLFLERVYGIETQELFYKLLERAFPLDLRA	2625	Qy	3642	FAGREQLVQHCORFLKMSQODVABEFAKTQTLTPDKIDPADENSWQHYLYSKLGSKS	3701
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Qy	2626	ATMLRNDCESSDMSALSMNRYTGNSTLPLLIKHAFYNEAENYASLLDALTHTVRLSKN	2685	Qy	3702	SNITVETAEAKAKI-----IDDTVERIVAMSKVLFGLHMDHPQMSKNVRSVVS	3752
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Qy	2686	RMLTKQREAVSDFVALTSQMPAMLLKRLKLTVDVSKLSEYTTVALRLLTLHYERCA	2745	Qy	3753	TQRKAVTACFRQTSLSLPHRACNIPARTYIELWLEENIGORVWLEDLTQSFEDEL	3812
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Qy	2746	KYVGSTGAGGAFGASSDEKRLTMMLFNIFDSLSKMDYBEPFLFKALPCLIIATGCAIP	2805	Qy	3813	KKSDVVEBEGEPDPLTQVTTCRGAMTERSGALQEDPLYNYSYAHIIAKSCGEBEEBEGG	3872
Db	2733	KYVGST--QOGSYGASSDEKRLTMMLFNIFDSLSNMDYDPFLFKALPCLIIATGCAIP	2791	Db	3801	SKKEGETTSKPDPLTQVTTCRGAMTERSGALQEDPLYNYSYAHIIAKSCGEBEEBEGG	3860
Qy	2806	PDYLSKNVDDEYKQAGADLDNPOYDOPINTSSVALNNDLNTIIVOKFSEHYHDWA	2865	Qy	3873	BEKEGGBAEAEDEGRASIEHEQEMEKQLLPHQARLADRGVAEMVLLHISASKGIPSENV	3932
Db	2792	PDYLSKNVDDEYKQAGADLDNPOYDOPINTSSVALNNDLNTIIVOKFSEHYHDWA	2849	Db	3861	BE--GGEGBEGEG--TSIHEQEMEKQLLPHQARLADRGVAEMVLLHISASKGIPSENV	3916
Qy	2866	SRKIENGWYVGEWSDSQKTHPRILKPYNNMLNDYKERYKEPVRESLKALLAIGWSVEHSE	2925	Qy	3933	MKTLOLGISILRGGNIDITOMGLNHLKOKKOVGFPTSITAGLMNSCSVLDDLAFAERNTKAE	3992
				Db	3917	MTTLNLGAILRGGNIDITOMGLNHLKOKKOVGFPTSITAGLMNSCSVLDDLAFAERNTKAE	3976









Db 4738 ACLSLVSLAMLIAIYHLLKVLPLAIPKREKEIARLRLEFEGLFIAEQPEDDDFKSHWDKLV 4797  
Qy 4803 SAKSPVNVWDFKVKVYKRAKYSEYDFDSISNMLGMEKTSFSQAEEBGSGLIHYINI 4862  
Db 4798 SAKSPVNVWDFKVKVYKRAKYSEYDFDSISNMLGMEKTSFAAQESE-ETGIFKYNWI 4856  
Qy 4863 DMYQVWQAGVITITNSFLYSILWYFSFSGMGNFNNFFFAAHLDDVAVGFKTLRTILQSVT 4922  
Db 4857 DMYQVWQAGVITITNSFLYSILWYFSFSGMGNFNNFFFAAHLDDVAVGFKTLRTILQSVT 4916  
Qy 4923 HNGKQLVUTVMTLLTIIVYIVIAENFRKFVQBEDDEVNRNCHDMLTCFVFNLYKQVR 4982  
Db 4917 HNGKQLVUTVMTLLTIIVYIVIAENFRKFVQBEDDEVNRNCHDMLTCFVFNLYKQVR 4976  
Qy 4983 AGGGTGELEPPDGDSEVYRIIPDISPFFFTIIVILLAILQGLIIDAFCGLRDLQESVKE 5042  
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Qy 5043 DMESNCFICGINKDYFDKVPYHGFTHVQREHNLANYMFFLMHLINKPDTYTGQTYVYN 5102  
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Qy 5103 MYQRCWDFPVPVGDGCFRQYED 5124  
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RESULT 10  
US-10-668-767-10  
; Sequence 10, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 5109  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-10-668-767-10

Query Match 79.6%; Score 21326; DB 4; Length 5109;  
Best Local Similarity 79.0%; Pred. No. 0;  
Matches 4081; Conservative 450; Mismatches 527; Indels 108; Gaps 40;  
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Qy 61 SQCFVIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILRHNSDMYLACLS 120  
Db 60 SQCFVIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILRHNSDMYLACLS 119  
Qy 121 SSSQDKLAFDVLGQHQSEACWTLHPASKORSEGEKVRVGDGLTVSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVLGQHQSEACWTLHPASKORSEGEKVRVGDGLTVSVATERYLHTTK 179  
Qy 181 ENEVSVIWNASFVHTWHSVOPYGTGIRMKYVGVFGDVLRFPHGGDECLTIPSTWTKDG 240  
Db 181 ENEVSVIWNASFVHTWHSVOPYGTGIRMKYVGVFGDVLRFPHGGDECLTIPSTWTKDG 240

Db 180 ENEOSIVNAGSFVHTWHSVOPYGTGIRMKYVGVFGDVLRFPHGGDECLTIPSTWGBEA 239  
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Qy 361 KSVETTKKGVKVEKQAILHEEGKDDGLDFSRSQSEESTARVIRKCSLSLTKFNGL 420  
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Qy 721 DGAYLWSGGRKTPNRTFAEBPYIRKGDVIGCCALDLTVPIINFMFNGVRVTSFTNENLE 780  
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Db 780 GMFFPVSICSSKLSRFLGEGHGRVAAPEGSPLVESLIPQOILSLEPCFYFNGLSK 839  
Qy 841 RALAGPPLVQDDTAFVPTFVDTLQITLPTTYVEQIRDKLAENIHEMWAANKIEAGHWGQH 900  
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Db 1080 TYRAKYNVANSKGYFEFEILLTAGPMRVGHADMAKPMMLGODENSWAGDYNKEKYV 1139  
Qy 1141 SGNTEFCQKONAVGVDVGVFLDLIDKTIISFSLNGELLDALGGETTFADV--QGDNFVPA 1198  
Db 1140 SGNTEFCQKONAVGVDVGVFLDLIDKTIISFSLNGELLDALGGETTFADV--QGDNFVPA 1199  
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Db 1200 CTLGVGQKARLTGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKQDIPFNTDEM 1259  
Qy 1259 IDTRIDVTRIPAGSDTTPCLKISHNTFETMEKANWFEFLRLSPVICHNEFFIDEAKARRW 1318  
Db 1260 IDTRIDVTRIPAGSDTTPCLKISHNTFETMEKANWFEFLRLSPVICHNEFFIDEAKARRW 1319







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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22563
; LENGTH: 5107
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-22563

Query Match      79.4%; Score 21270.5; DB 6; Length 5107;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 4070; Conservative 448; Mismatches 522; Indels 121; Gaps 40;

Qy 22 MVLCSCTATGRRVCLAAAGFGNRHCFLENIADKNIPDLSOCVFVIEQALSVRALQELVT 81
Db 1 MVTLSCTATGRRVCLAAAGFGNRHCFLENIADKNIPDLSOCVFVIEQALSVRALQELVT 60
Qy 82 AAGSETGKTGSGHRTLLYGNAILLRHLNSDMYLACLSTSSSQDKLAFDVGLOQHSQGEA 141
Db 61 AAGSETGKTGSGHRTLLYGNAILLRHNSDMYLACLSTSSSQDKLAFDVGLOQHSQGEA 120
Qy 142 CWTWLPASKORSSEGEKVRVGDDLLILSVATERYLHTTKENEVSIVNASPHVTWHSQPY 201
Db 121 CWTWLPASKORSSEGEKVRVGDDLLILSVATERYLHTTKENEQSIVNASPHVTWHSQPY 180
Qy 202 GTGISRMKYGVGVGGDLVRFPHGGDECLTIPSTWTKDGGONIIVYEGGSVMSQARSILWR 261
Db 181 GTGISRMKYGVGVGGDLVRFPHGGDECLTIPSTWGREAGQNIIVYEGGVMAQARSILWR 240
Qy 262 LELARTKWAGGFINWHPMRIRHTTGRYLGVNDQNELYLVSREEAATTASCAFLRQEKD 321
Db 241 LELARTKWAGGFINWHPMRIRHTTGRYLGVNDSNELILVKKEASTATTTFCRLQEKD 300
Qy 322 DOKQVLEKDLLEVIGAPIIKYIGDSTVIIVQHSETGLWSYKSYETKKKGKVGKVEKQAILH 381
Db 301 DEKKVLEKDLLEVIGSPIIKYIGDSTVIIVQHCETSLWSYKSYETKKKGKVGKVEKQAILH 360
Qy 382 BEGKMDCLDFRSQEEBSRTARVIRKCSLFTFKINGLETLOENRRHSMFFASVNLGEM 441
Db 361 BEGKMDCLDFRSQEEBSRTARVIRKCSLFTFKITALETLOENRRHSHIFPKVNLNEM 420
Qy 442 VMCLEDLNYFPAQPEDMEHEKQNKFRALNRQDLFOEEGILNLEAIDKINIVTSQ 501
Db 421 VMCLEDLNYFSQPEDMEHEKQNRFEALNRQDLFOEEGVNLLEAIDKINIITSQ 480
Qy 502 FLAGLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGE 561
Db 481 FLAGLAGDETCQSDILSTLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASSE 540
Qy 562 GTGMLDVLHCVLIDSPEALNMRDEHIKVIISLLEKKGDRPKVLDVLCSCVGNQAVRS 621
Db 541 GSGMLDVLHCVLIDSPEALNMRDEHIKVIISLLEKKGDRPKVLDVLCSCVGNQAVRS 600
Qy 622 SONNICDYLLPGKNLLQTLADVHSSVRPNI FVGRVEGSAVYRKWYFEVTMDHIEKTH 681
Db 601 SONNICDPLPGKNLLQTLADVHASIRPNI FVGRVDGSSMYKWYFEVTMDHIEQTH 660
Qy 682 MPMHLRIGWANTGVYVPGGGEKXGNGVGGDDLYSYGFDGAYLWSGGRKTPVNRTHAE 741
Db 661 MPMHLRIGWANTGVYVPGGGEKXGNGVGGDDLYSYGFDGAFLLWLGGRKTLVVDALPEE 720
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Db 721 PFIRKGDVIGVAILDSVPIITFTFNGVKVRSFDFNLDGMFFPVMSCSSKLSCRFLFG 780
Qy 802 EHGRLRYAAPGSGYPLVBSLLPQQTLSLEPCFYFGNLSKRALAGPPLVQDDTAFTVPTVD 861
Db 781 DHGRLKFPAPMGFSALVQCLPQQTLSLDPFCFYGNLAKVNLAGPWLIEDTAFTVXPVD 840
Qy 862 TLQITLTPYVQIRDKLAENITHEMWAMNKIEAGMWYQDQREDLHKHICLPVFFERLPAAE 921
Db 841 TTGVTLPSSVDQIKELAEINITHEMWALNKIEAGWSGSHRDDYHRIHPCLTHTPEKLPAAE 900
Qy 922 KRYDQLAVQTLTKTIISLGYIITMDKPPAIRPVRLPNEIFMQGNGYKYPAPLDLSAVTLT 960
Db 901 KRYDQLAVQTLTKTIISLGYIITMDKPPAIRPVRLPNEIFMQGNGYKYPAPLDLSAVTLT 960
Qy 982 PKWDELVDQLAENTHNLWABERIQOQWTYGLNEDSDMHRSPHLVPYPKVDDAIKKAURDT 1041
Db 961 PKLEELVDQLAENTHNLWABERIQOQWTYGLNEDSENHRSPHLVPYAKVDEAIKKAURDT 1020
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Db 1081 LTSGPMRVGWAHADMAPGMMLGSEDTSWAFDGHNVTKMHAGSIEHFVGVYEAAGVGCFI 1140
Qy 1162 DLIDKTIISFSLGELLMDALGGETTADY--QGDNFVPACTLGVGQKARLYTYGQDVNLLK 1219
Db 1141 DVKEQTIISFSLGELLMDALGGETTADYTAEGVGFVPACTLGVGQKARLYTYGQDVNLLK 1200
Qy 1220 YFTTCGLQEGYEPFCVNMKRDVTHWTKQOPIFENTDEMIDTRIDVTRIIPAGSDTPPCLK 1279
Db 1201 FFTTCGLQEGYEPFCVNMRRPVTHWTKQOPIFENTDEMPDCRIDVTRIIPGADTPPHLK 1260
Qy 1280 ISHNTFETMEKANWFLRLSLPVI CHNEFIDEAEKARRWVEIKDRQOILMKEA-VEAQM- 1337
Db 1261 ISHNTFETMEKANWFLRLSLPVTCHGEFISEQEKARRWDEIKNUQVRLMREAEIAAQMQ 1320
Qy 1338 ----PAHIDIMRSGFTMDIKGLHYE-DNQEELPSSMKRLPSRPPRKSMTRGVTIQN 1392
Db 1321 VQTAAAHMDHMLKGFGNMNDIKGLTRNFDEHADAEADHMRGNRPPRKSLSLTENIT--- 1377
Qy 1393 YNNLQCVNGVNGHRSSTSEAEWAKYDLCAGQLTPDDKKDKRGRPPFKFRKRGESSDRAK 1452
Db 1378 FETDMSAALDEMORST-----VLDNMGLEEMDDKK-KRGRSPFKFF-SKSRDQREK 1430
Qy 1453 SRKSKTPDPDSETPESPERGARRPNQIKVSOANQRNGNMARPSRTNLVYSGVGLNMAT 1512
Db 1431 -MGARTLDTSLERRNTVAHGRNVVNQMTTTRAPTLRLNNAEIPSPV----- 1476
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Db 1477 -PQGPQLSGSNLQGPVETSGDEMDAECLKLINEFYGVRIYPGDPTHVYVWTTQ 1535
Qy 1573 YHLHSDFNOSKVTYKSSVIITDDYDRVVENNRQSCVMYRADELNYEVMAEATKAGASQ 1632
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Db 1716 VSMALHAPIPEEDRCIDILEPIEMDKLLSFHSHLTLTYAALCYOSNYRAAALCHQVQKQ 1775
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Db 1776 LLYAIRSEYNSGMLRQCFYDLLIALHLESHATTMEVCKNEVITPLGAELKELYDEEMQH 1835
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Qy 1919 LAEAVETNOVHNRPVCGSNENLFLPLIKLVDRLLVGMWRDEVEKLLIWTNTPEDDPS 1978
Db 1896 LKDAVEINQVHNRPDIQWNTNENLFLPLIKLUTDRULLVGLTDEVDQRLVWIDPETWQA 1955
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Db 4218 MDFLACCERNHEGKIDYRAFVEHFHEPSKEIGFNLA VLLNLSEHMPNEPRLARFLETA 4277  
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Db 4278 GSVLNYPEPFLGRIEILGSSKRIERVYFEIKSDNIEQWEKPOIKESKRAFPYSIVTGGD 4337  
Qy 4360 KEKLEAFVNFCEDAIFEMTHASGLMAAEEESVGGTKNREASY-NYMGDDDDDERACKDPFR 4418  
Db 4338 KEKLEAFVNFCEDAIFEMTHASGLMATDDG--GGNVKRDYATSSYMSSEEEERARPIR 4395  
Qy 4419 RGLQSVKDGVATAFSSLSPSNIKAKIADMOMQMPAELAVGFFKMFYLYFYLVGVLVVV 4478  
Db 4396 RTITAVKEGLKFGVHMLSPANIKHQIGVMQTKSIPELIVGFFKIIFYFYVYGVAFPCV 4455  
Qy 4479 RYIFGVLLGMRGPOTDEPPPEPTEEEKIGQLRHRLLATQSSRHLPALPPADDTGOMQVS 4538  
Db 4456 RYIFGILLNLMRGPAPEQEEEPVVEETFG-----RALPPLPUEEPPTGVO-- 4501  
Qy 4539 AFGDLITKEDNGOIQVKPHEPSTSTSPSGEAEVSPDESADHTEE-----QRPPSLI 4591  
Db 4502 AFGDLINKENGMKYVVVHESPANSMEEGES--SPEDGAAAGELVEGEPHEPISIV 4559  
Qy 4592 DLLGGEQAKQAQERMEAAQAQAAMSIAEASKAVQGPAPS-ALSOVDLSQYTRRAVS 4650  
Db 4560 DLLGGEAAKAAQERQEAQKAQAAMASIEAEAKSSAPQETPAVHQIDFSQYTHRAVS 4619  
Qy 4651 FLARNFYNLKVALVLAFCINFLVLLFYKVTILDSEGGSGGLGIIAGGGSGSAC--GS 4707  
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Qy 4824 YSETYDPSISNMLGMEKTSFAQEEBSKGLIHYIINIDRYQWKAGVITONSFYS 4883  
Db 4799 YSETYDPSISNMLGMEKTSFAAQAQEE--ETGIFKYIMNIDRYQWKAGVITDNALYS 4857  
Qy 4884 LWYFSFVGMGNFNFPPFAAHLDDVAVGPKTLRTILOSVTHNGKQLVLTVMLLTIIIVYIT 4943  
Db 4858 LWYFSFVGMGNFNFPPFAAHLDDVAVGPKTLRTILOSVTHNGKQLVLTVMLLTIIIVYIT 4917  
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Db 4978 IIFDITFFFFVIIILLAIIOGLIIDAFCGLRDQLESVKVDNMESNCFICGINKVDFDIYPH 5037  
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Db 5098 D 5098

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; GENERAL INFORMATION:

; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
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; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
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; CURRENT FILING DATE: 2003-09-23  
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; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 125  
; LENGTH: 5112  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: gi 2160477  
US-10-668-767-125  
  
Query Match 79.2%; Score 21234.5; DB 4; Length 5112;  
Best Local Similarity 78.8%; Pred. No. 0;  
Matches 4072; Conservative 441; Mismatches 546; Indels 109; Gaps 41;  
  
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Db 1 MAEAGG-SQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRRHCFLENIADKNIPDDL 59  
Qy 61 SQCVFIEQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLS 120  
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Db 120 SSSNDKLUSFDVGLOQHSQGEACWMTVHPASKQSEGEKVRGDDLIILVSVATERYLHTTK 179  
Qy 181 ENEYSIVNASFHVTHMSVQPYGTGIRSMKYGVYVFGDVLRFPHGGDECLTIPSTWKG 240  
Db 180 ENEYSIVNASFHVTHMSVQPYGTGIRSMKYGVYVFGDVLRFPHGGDECLTIPSTWGRE 239  
Qy 241 GQNIIVTEGGSVMSQARSRLRLELARTKWAGGFINTWHPRIHRTTGRYLGVNDQNELY 300  
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Db 359 KSYETKKKGKVEEKQAILHEEGKMDCLDFSRQSEESKARTARVIRKCSLFTKFNGL 418  
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Qy 481 EGTILNLLEAIDKINVTISQGLAGFLAGDSQSWEMISGYYQLLAAAIKGNHTNCAQ 540  
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Qy 541 FANSNRLNWLFSRLGSAQSGEGTGMCLDLVLCVLDLSPALNMMDHEIKVIISLLEKHGR 600  
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Qy 601 DPKVLDVLCISLCVNGVAVRSSQNNICDYLPGKNLLQTLALVDHVSVRNIFVGRVGE 660  
Db 599 DPKVLDVLCISLCVNGVAVRSSQNNICDYLPGKNLLQTLALVDHVSVRNIFVGRVGE 658





Db 2791 PDYSLSKNTDEBYCRQWAP--DQPYMPNPIDTNNVHLNDLNSLVQKPESEHYHDWA 2848  
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Db 2849 SRLEGGWTYGDIRSDNDKHPRLKPYNMLSEYERERYRDPVRECLGALLAIGTWVHSE 2908  
Qy 2926 VDI FSNRRSSNRRQSKSGRRPEI--VTDSATPDYDYPNHPVDMNTNLTLSREMOMAEELA 2983  
Db 2909 VEPFLNHRGSTRROSK-----POINEFQNEGSPFNYPNHPVDMNSLNTLSREMOMAEELA 2963  
Qy 2984 DNAMDIAWAKKEELVNTGGGHPOLVPYDILLTQKEKKKDREROEFLKYLOYGYKLRH 3043  
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Qy 3044 PSKAPQSDTEQTGTGVAIELRFAYSLSLEKLIQYIDRATINNKLKLPSTFSRRSSPKTST 3103  
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Qy 3404 GPDNVPTGGNHVMTVAEHNQQLKNVLKLIKKNIGNENAPMWTIATYTOQIIINSSE 3463  
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Qy 3464 ELLRDSFLPLAERYKRTDNMFHKEESLRGFIKSTDDTSQVESQIQEDWOLLVRDIYSF 3523  
Db 3443 ELLKDPFLPLAERYKRTENMLHKEDSNRGFIK SATDDTSQVETQLQEDWMLLVREDIYSF 3502  
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Qy 3584 LIMPTATRRVTAVDGTPQGGG--KKKKKHRDKRDKDKEYQASLMVACLKRLLPVGLNL 3641  
Db 3563 LIMPTATR-SAISGAPVAGVKYKKKKRDKRDKDKEYQASLMVACLKRLLPVGLNL 3621  
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Db 3622 FAGREQLVQHKORYLKMPEDYIEFARNQLTLPDKLDPSEMSWOHLYSKLG-KTE 3680  
Qy 3702 SNIIVETAENKAKI-----IDDTVERIVAMSKVLFGHLMDHPQMSKNYRSVVS 3752  
Db 3681 EPVD-EQALEKANVNSNEKGDKTQETVDRI VAMAKVLFGLHMDHPQMSKNYRSVVS 3739  
Qy 3753 IQRKRAVIACFRQTSLSHLPRHRACNIPARTYYELWLBEENIGOVMIEDITQSFDAEL 3812  
Db 3740 IQRKRAVIACFRQTSLSHLPRHRACNIPARSYYEQMLQEENVGVQVVEDLTQTFEDSEK 3799  
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Db 3800 SKKEGEETSDSKPDLTQLVTTFCRGAMTERSGALQEDLLYSYAQIAAKSTGKEEBEGG 3859  
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Qy 4053 DYLLRLQESIMDFYHYSSKELIDPAGKANFFKAIGVASQVFNTLTLEVI QGPCTNQOAL 4112  
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Db 4096 AHSRLMDVAGGFTPLFSHMQDKLSKUSSQVDLLKELLNLQKDMI TMMLSLMEGNVNGTI 4155  
Qy 4173 GKQWDTLVESASNVLELILKYFDMFLKDLTSSASQFQIDANNMGVLPKDKKMEQEQ 4232  
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Qy 4532 TGMQVSAFGLDITTKEDNGOI QVKPHESPSTSPSSGEEAEVSPDESADTBE----- 4584  
Db 4502 PGTVQ--AFGLDINKENGMYKVVHESPANSSWEEGES--SPEDGAASAGELVEGEPH 4557  
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Qy 4644 YTRAVSFLARNPYNLYKVALVLAFCINFVLLEYKYVSTLDGEGEGSGLDIIAGGSGS 4703  
Db 4618 YTHRAVSFLARNPYNLYKVALVLAFCINFVLLFYKVTSFT-EEADSSAEBELIGSGSG 4676  
Qy 4704 GA---GS--GSGDGGESGE-DDDALEVVIHIDDFYMEHVIMKAAVLSHSIVSLAILIG 4756  
Db 4677 GADITSGFGSGSGSGSGDGENEDEPELVVHVEDDFYMEHVLRACLSLSVSLAMLIA 4736  
Qy 4757 YYHLKVPALAI FKRKEIARLEFDGLYIABQPEDDDDLKSHWDKLVISAKSPVNVWDKFV 4816  
Db 4737 YYHLKVPALAI FKRKEIARLEFEGLFIAEQEDDDDPKSHWDKLVISAKSPVNVWDKFV 4796  
Qy 4817 KKKVRKYSTYDPSISNMLGMEKTSFSAQBESESGKLIHYIINIDWRVQVWKAGVTIT 4876  
Db 4797 KKKVRKYSTYDPSISNMLGMEKTSFSAQBESESGKLIHYIINIDWRVQVWKAGVTFT 4855  
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QY 4997 DDSEYRIIFDISFFFFIIVILLAILOGLIIDAFAELRDQLESVKEDMESNCFICGINKD 5056  
DB 4976 DDYEVYRIIFDITFFFFIIVILLAILOGLIIDAFAELRDQLESVKDNMESNCFICGMGKD 5035  
QY 5057 YFDKVPHGFDTHVQREHNLANMFFLMHLINKPDTETGQTYVNMVYQRCWDFPFGVD 5116  
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QY 5117 CFRKQYED 5124  
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RESULT 13  
US-10-668-767-56  
; Sequence 56, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Libong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 5126  
; TYPE: PPT  
; ORGANISM: Drosophila melanogaster  
US-10-668-767-56  
Query Match 79.2%; Score 21218.5; DB 4; Length 5126;  
Best Local Similarity 78.6%; Pred. No. 0;  
Matches 4072; Conservative 442; Mismatches 545; Indels 123; Gaps 42;  
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QY 61 SOCVFVEIQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLSL 120  
DB 60 SOCVFVEIQALSVRALQELVTAAGSETGKGTSGHRTLLYGNAILLRHNSDMYLACLSL 119  
QY 121 SSSQDLAFDVLGLOHSGEACWHTLHPASKORSEGEKVRVGDDLLVSVATERYLHTTK 180  
DB 120 SSSNDKLSFDVLGLOHSGEACWHTVHPASKORSEGEKVRVGDDLLVSVATERYLHTTK 179  
QY 181 ENEVSIVNASFHVTHWSVQPTGTSIRMKYGVYFGDVLRFPHGGDECLTIPSTWKDG 240  
DB 180 ENEQSIVNASFHVTHWSVQPTGTSIRMKYGVYFGDVLRFPHGGDECLTIPSTWGRE 239  
QY 241 GQNVVYEGGSVMSQARSRLRLARTKWAGGFINWHPMRIRHITTGRLGVNDONELY 300  
DB 240 GQNVVYEGGSVMSQARSRLRLARTKWAGGFINWHPMRIRHITTGRLGVNDONELY 299  
QY 301 LVSRREATTASCAFCLROEKDQKQVLEDKLEVGAPIIKYGDSTVIVQHSETGLWSY 360  
DB 300 LVYKGEASTATTFSH-QEKDEKKVLEDKLEVGSPILKIGDITVIVQHSETGLWSY 358  
QY 361 KSYETKKGVGVKEEKQAILHEEGKMDGLDFSRSOEESRTARVIRKCSLSFTKPFINGL 420  
DB 359 KSYETKKGVGVKEEKQAILHEEGKMDGLDFSRSOEESRTARVIRKCSLSFTQFITAL 418

QY 421 ETLOENRRHSPFASVNLGEMVWVCLDLINYPAQPEDMEHEHEKONKFRALNRQDLFOE 480  
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QY 481 EGIINLILLEAIDKINVTISQGFAGLAGESQGWEMISGYLYQLLAAIIGKHNINCAQ 540  
DB 479 EGVNLNLLEAIDKINVTISQGFAGLAGESQGWEMISGYLYQLLAAIIGKHNINCAQ 538  
QY 541 FANSNRLNWLFSRLGSOASGEGTGMLDVLHCVLIDSPEALNMMRDEHKVILSLEKHGR 600  
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QY 601 DPKVLDVLCISLVGNGVAVRSSQNNICDYLLPGKNLLQTLALVDHVSVSRPNIFVGRVGE 660  
DB 599 DPKVLDVLCISLVGNGVAVRSSQNNICDYLLPGKNLLQTLALVDHVSVSRPNIFVGRVGE 658  
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QY 841 RALAGPVLQDDTAFVTPVDTLOITLPTVYVQIRDKLAENIHMMWANKTEAGWMYGDQ 900  
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QY 1319 VEIKDROQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371  
DB 1319 VEIKDROQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1378  
QY 1372 KRLPSRPRKSGMTRGVTIQNNNLQPGQVNGMHRSTSEAEWAKYDLAGOGLTPDQKDK 1431  
DB 1379 MRGNRPRKSGMTRGVTIQNNNLQPGQVNGMHRSTSEAEWAKYDLAGOGLTPDQKDK 1429  
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Db 1534 GVRIFPQDPHPHYVWTTQYHLHSHREFNKNKVRGSVIEDDYEMAIERDQSCYV 1593
Qy 1612 RADLYNEVWABATAKASQGMFTGCSVDSTSGSVSTCGKDTSPFKMEPETKLPPAI 1671
Db 1594 RADELNEVTQDASGKASQGMFVGCFTDGTATGIIRFTCEGKOTSHRMMEPDTKLPPAI 1653
Qy 1672 FVEATSEIILQIEIGRATSPLSAALPTSDKHVIOQFPPLKVOCLKPHQWARVNOS 1731
Db 1654 FVEATSEIILQIEIGRTPPTPLPSAALPTSDKHINQSPPLKVOCLRPHQWARVENTA 1713
Qy 1732 LQVHALKSIDIRGWSMLCEDAVSMALHIPEEDRCIDILEPIEMDKLLSFHSHLTLYAA 1791
Db 1714 LQVHALKSIDVRGWSMLCEDPVSMALHIPEEDRCIDILELIEWMLLSFHAHSLTLYAA 1773
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Db 1774 LCYQSNVRAAHALCOHVQKOLLYAIRSEYMSGRLRGQFYDILLJIALHLESHATTMEYCKN 1833
Qy 1852 EFVILPGLKALYEEPDMGHSLRLOTESVRPQMKWTDI-----AESITE 1897
Db 1834 EYITPLGAELKELYSDEMQHSLSLVTESVRPOLRMTETITPPVIATSSMPSVSSEFIPD 1893
Qy 1898 ISNLYSPYFPLEVAREFVMOALABAETVQNHNRDPVGGSENILFLPLIKLVRDLLEVGM 1957
Db 1894 IDQLYSPKFLLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENILFLPLIKLDRLLLVGV 1953
Qy 1958 MRDEBVKLLIMTNPETWDPSPFVKGDEHRKGLLHMKWABGAKLQWCYLLLOHLNDLOLR 2017
Db 1954 LTDEVDORLLVMDPETWQAFEREGKDEHRKGLLTKWABGAKLQWCYLLHLHYDTQLR 2013
Qy 2018 HRVEAITAFADHFVGDLOTDLRYTELKQSDLPASAANKTREFRCPPREQWNAILSPK 2077
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Qy 2078 HLEEDKENCPCGBELLARMNEFHDITMAHYSLHALQEPDAAENQOE-PEAKPAGFKLYN 2136
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Qy 2137 IINTVKELEESAKAIEBPBKTPBEKFRKVLIOITVNWABESQIETPKLVREMPSSLVRQ 2196
Db 2134 FINTVKELEEGKEVEBPBKTPBEVFRKVLIKTIVSWABESQIENPKLVREMPSSLVRQ 2193
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Db 2194 YDTVGEIVRALKTYVINTRARDDAEMWVGLSOIRALLPVQMSQEBEELMRKELKLVN 2253
Qy 2257 NHTFQHPDLIRLVLRVHENVNVMNMTILGRAQAQSDAQSPSSQPAVE--DSKEKDTSHM 2314
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Db 2433 VEENANLVIRLLIRREPCLPALGEGEGGLFRAIVEANRMSERISDRCKQD-BAEGTIA 2491
Qy 2494 --NFSHPLEPDEDEDYIDTGAAILNFYCTIIVDILGRCAPDAGVIALGKNESLARAILR 2551
Db 2492 GLNFTPLPEGEDEDYIDTGAAILNFYCTIIVDILGRCAPDASVIEQGNESLARASLR 2551
Qy 2552 SLVPLEDLQGLVLSKFTLSQTAPGEEKPKSDMPDGLPNNKQISVLFLERVYGEAQDLF 2611

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Qy 3090 STTFSRRSPKTRDIPKFSKAVLPLMEKYFSTRNYFIAVATATNNVGAASLKEKEMV 3149
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Qy 1372 KRLPSPRPKSGMTRGVTIQYNNLPQGVNGMHRSTSEAMAKYDLGAOGLTDPDDKKOK 1431  
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Db 1834 EYITPLGAELKELYSDEEMOHSRLSVTESVRQLRWTEITPVPVIATSSMPSVSSEPIPD 1893  
Qy 1898 ISNLYSPYFPLEVAREFVMOALABAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957  
Db 1894 IDQLYSPKPFLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1953  
Qy 1958 MRDEDEVKLLIMTNPETWDFSPKGEKDEHRKGLLHMMAEGAKLQMCYLLLOHLNDIQLR 2017  
Db 1954 LTDDEDVQRLLVMDIPETWDOAFEREGKDEHRKGLLTMMAEGAKLQMCYLLLHHYDITQLR 2013  
Qy 2018 HRVEATIAPAHDFVGDLQDQLRRTYIKOSDLPASAANKTREFRCPPREOMNAILSFK 2077  
Db 2014 HRVESIIAFSHDFVGDLQDQLRRTYIKOSDLPASAANKTREFRCPPREOMNAILCFCF 2073  
Qy 2078 HLBEEDKENCPCGEEIATARNNEFHDITLMAHVSJLHALQEPDAAENQEB-PEAKPGAFGLYN 2136  
Db 2074 NLEPDQDNCNCTGLEGRLGRGLDFHDSLMQKVSLNALQEPDGVGTAIEEVKGTGPIITKYN 2133  
Qy 2137 IINTVKELEBEAKAIEBPPPKTPEEKFRKVLIOITIVNMAESQIETPKLVREMFSLVRQ 2196  
Db 2134 FINTVKELEBGPKEVEPEKKTPEEVRKVLIKTIVSWABESQIENPKLVREMFSLLRQ 2193  
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMVGLSOIRALLPVQMSQEBEELMRKELWLKN 2256  
Db 2194 YDTVGELVRALEKTYVINTEARDVDAEMVGLSOIRALLPVQMSQEBEELMRKELWLKN 2253  
Qy 2257 NHTTFQHPDLIRVLRVHENYMAVMNMTLGRRAQASDAQSSQPVAB--DSKEKDTSHEM 2314  
Db 2254 NATTFQHPDLIRILRVHENYMAVMNMTIGRRAQASDA-PTQSEVAREGAPSKEKDTSHEM 2312



Db 4454 GFFKIIYIFYYTGAFVCVRYIYIFGILLNLMRGPAEQEBEPPVVEBETFG----- 4504  
Qy 4518 QSSRHLPALPADDTGQMQVSAFGLDITKDNGOIQVKPHESPSTSTPSSGEEAEVSPDE 4577  
Db 4505 ---RALPPLPEEPGTVQ--AFGLDINKENGMYKVVVHESPANSSMEEGES--SPED 4557  
Qy 4578 SADHTEE-----ORPPSLDILGGCAKQAOERMEAAQAOQAASATAEASKVAVQG 4630  
Db 4558 GAASAGELVEGEPHQEPTISIVDLGGEAAKAAQOEQAQAQAANASTAEAAKSSSA 4617  
Qy 4631 PAPS-ALSOVDLSQVTRAVSFARNFNLKYVALVLAFCINFVLLFKYKSTLIDGEGEG 4689  
Db 4618 POETPAVHQIDFSQVTRAVSFARNFNLKYVALVLAFSINFMLLYKYKTSFT-READS 4676  
Qy 4690 SGLGDIIAGGSGSGA---GS---GSGDGSERGE-DDDALEVVIHIDEDFFYMEHVIKMA 4742  
Db 4677 SAEELILGSGSGGADITGSGFGSGDGGSGDGEDEIPELVHVDEDFYMEHVILRIA 4736  
Qy 4743 AVLHSIVSLAILIGYHYHLKVP LAIFKREKETARKLEFDGLYIAQOPEDDOLKSHWDKVI 4802  
Db 4737 ACLHSLVSLAMLIAYHYHLKVP LAIFKREKETARKLEFEGLFIABQPEDDDFKSHWDKVI 4796  
Qy 4803 SAKSFPVNYWDKFKVKVRAKYSTYDFDSTSNMLGMEKTSFSAQEEGSKGLIHYINI 4862  
Db 4797 SAKSFPVNYWDKFKVKVROKYSITYDFDSTSNLGMKSTFAAQESE-ETGIFKYIMNI 4855  
Qy 4863 DWRQVQWKAGVTITDNGFLYSLWTFVSVMGNFNFFFAHLLDVAVGFKTLRTILQSVT 4922  
Db 4856 DWRQVQWKAGVTITDNGFLYSLWTFVSVMGNFNFFFAHLLDVAVGFKTLRTILQSVT 4915  
Qy 4923 HNGQLVLTVMLLIIVYIVIAFNFRKPYQOEDEVDNRNCHDMLTCEVFNLKQVR 4982  
Db 4916 HNGQLVLTVMLLIIVYIVIAFNFRKPYIQEEDSEVDKCHDMLTCEVFNLKQVR 4975  
Qy 4983 AGGIGDELEPPDGDSDSVRIIFDISFFPIIIVLLAIQGLIIDAFAGELRDQLESVKE 5042  
Db 4976 AGGIGDEIGDPDGDDEYVRIIFDITFFPVIILAIQGLIIDAFAGELRDQLESVKD 5035  
Qy 5043 DMESNCITGINKNDYFDKVPHGFDTHVQREHNLANYMFFLMLINKPDTEYTGQSTYVN 5102  
Db 5036 NMESNCITGINKGDKDFDIPVHGFDTHVQKEHNLANYMFFLMLINKPDTEYTGQSTYVN 5095  
Qy 5103 MYTORCWDFFPVGDCFRKQYED 5124  
Db 5096 MYQORSWDFPVGDCFRKQYED 5117

RESULT 15

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; Sequence 126, Application US/10668767  
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; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
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; PRIOR APPLICATION NUMBER: 60/412,795  
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; SEQ ID NO 126  
; LENGTH: 5112  
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; ORGANISM: Drosophila melanogaster

; FEATURE:  
; OTHER INFORMATION: gi 2160478  
US-10-668-767-126  
Query Match 79.1%; Score 21191.5; DB 4; Length 5112;  
Best Local Similarity 78.6%; Pred. No. 0;  
Matches 4061; Conservative 450; Mismatches 548; Indels 109; Gaps 41;  
Qy 1 MAEAGGASEQDDVSFLRTEDMVLCTATGERVCLAAEGFGNRHCFLENIADKNIPDDL 60  
Db 1 MAEAGG-SEQDDVSFLRTEDMVLCTATGERVCLAAEGFGNRHCFLENIADKNIPDDL 59  
Qy 61 SQCVFIEQALSVALQELVTAAGSTGKTGSGHRTLLYGNAILRLHNSDMYLACLST 120  
Db 60 SQCVFIEQALSVALQELVTAAGSTGKTGSGHRTLLYGNAILRLHNSDMYLACLST 119  
Qy 121 SSSQDKLAFDVGIOQHSQSGEACWMTLHPASKQSRSEGEKVRVGDDLLVSVATERYLHTTK 180  
Db 120 SSSNDKLSFDVGIOQHSQSGEACWMTVHPASKQSRSEGEKVRVGDDLLVSVATERYLHTTK 179  
Qy 181 ENEVSVINASFVTHWSVQPYGTGIRMKVGVVFGDVLRFPHGGDECLTIPSTWKDG 240  
Db 180 ENEQSVINASFVTHWSVQPYGTGIRMKVGVVFGDVLRFPHGGDECLTIPSTWGRE 239  
Qy 241 GQNIIVYEGSVMSQARSRLWRLERLARTKAGGFINWHPMRIHITTTGRYLVGNQDNELY 300  
Db 240 GQNIIVYEGSVMSQARSRLWRLERLARTKAGGFINWHPMRIHITTTGRYLVGNQDNELY 299  
Qy 301 LVREBEATTASCAFLRQERKQVLEDKDLEVIGAPIIKYGDSTVIVQHSSETGLWSY 360  
Db 300 LVKKEASIAITTFSW-QEKDDEKVLKDEKLEIGVSPILIKYGDSTVIVQHSSETGLWSY 358  
Qy 361 KSYETKKKGKGVKEEQAAILHEEGKMDGLDPSRSEESRTARVIRKCSLFTKFNGL 420  
Db 359 KSYETKKKGKGVKEEQAAILHEEGKMDGLDPSRSEESRTARVIRKCSLFTKFNGL 418  
Qy 421 ETLQENRRHSFASVNLGEMVNCLEDLINYPADPEDMEHEKONKFRALNRQDLFOE 480  
Db 419 ETLQENRRHSFASVNLGEMVNCLEDLINYPADPEDMEHEKONKFRALNRQDLFOE 478  
Qy 481 EGIINLILAEADKINIVITSGFLAGFLAGDESQSWEMISCYLYQLLAAAIKGNHTNCAQ 540  
Db 479 EGIINLILAEADKINIVITSGFLAGFLAGDESQSWEMISCYLYQLLAAAIKGNHTNCAQ 538  
Qy 541 FANSRLNMLFSLGSOAGSGEGTMDLVHLCVILDSPEALNMRDEHIKVIISLLEKXGR 600  
Db 539 FANSRLNMLFSLGSOAGSGEGTMDLVHLCVILDSPEALNMRDEHIKVIISLLEKXGR 598  
Qy 601 DPKVLDVLCSCVGVAVRSQNNICDYLPGKNLLQTLALVDHVSSVRPNIPVGRVGE 660  
Db 599 DPKVLDVLCSCVGVAVRSQNNICDYLPGKNLLQTLALVDHVSSVRPNIPVGRVGE 658  
Qy 661 SAVYRWYFEVTHDHIKTHMMPHLRIGWANTTGVYVPGGKGKMGNGVGDLYSYGF 720  
Db 659 SSMYQKRYFEVTHDHIKTHMMPHLRIGWANTTGVYVPGGKGKMGNGVGDLYSYGF 718  
Qy 721 DGAYLMSGGRKTPVNRTHAEEPIYRKGDVIGCALDLTVPIINFMFNGVRVGTSTNNLE 780  
Db 719 DGAYLMSGGRKTPVNRTHAEEPIYRKGDVIGCALDLTVPIINFMFNGVRVGTSTNNLE 778  
Qy 781 GMEFPVITSSKSLSCRFLLGGEHRLRYAAPEGVSPILVESLIPQIILSLPCFVFGNLSK 840  
Db 779 GMEFPVITSSKSLSCRFLLGGEHRLRYAAPEGVSPILVESLIPQIILSLPCFVFGNLSK 838  
Qy 841 RALAGPPLVQDDTAFFVTPVDVTLQITLPTVVEQIRDKLAENIHEHWMANNKIEAGMYGDQ 900  
Db 839 NVLAGPWLIEDDTAFVPKPVDVTTGVTLPSSVDQIKELAEINHEHWMALNKEACWSGEH 898  
Qy 901 REDLHKTHPCLVPPERLPPAEKRYDQLAVQTKLALGYIISLDKPPAIRNVRPLNE 960  
Db 899 RDDYHRIHPCLTHTFEKLPAAEKRYDQLAVQTKLALGYIISLDKPPAIRNVRPLNE 958  
Qy 961 PFMQSNQYKPAPLDLSAVTLTPKMDLVQDLAENTHNLWARERIQQOQVTCGLNEDSDMHR 1020



Db 959 IFMQNGYKPAFLDLSAVTLTKLEELVDQLAETHNLWABERIOQGWTYGLNDSSENR 1018  
Qy 1021 SPHLVPYKVDADAKKANRDFASETVRLLYGYMLDPTTGEQHEALLLEASKOKQADFR 1080  
Db 1019 SPHLVPYAKVDEAKKANRDFASETSANAPGLRICLGSSDGRNGGTSGRRPTQVRRIP 1078  
Qy 1081 TYRAEKNYAVSGKWYFEFEILTAGPMRVGWAHADMAPGMLGDENSWAFFDGYNEEKVY 1140  
Db 1079 TYRVERNAVTSKWYFEFEVLTSMPMRVGWARADCYFGMLGSEDTSWAFDGHNVTKOH 1138  
Qy 1141 SGNTESPKQWAGVGVGDFLDLDIKTTSFSLNGELLDALGGETTADV--QGDNFVPA 1198  
Db 1139 AGSIEHFGVREAGDVIGCFIDVKEQTISFSLNGELLDALGGETTADVTAEGVGFPA 1198  
Qy 1199 CTLGVGQKARLYTGODVNTLKYFTTCGLQEGVEPCVNMKRDVTHWYTKDOPIFENTDEM 1258  
Db 1199 CTLGVGQKARLYTGODVNSLKFFTTCGLQEGVEPCVNMRRPVTWYTKDOPIFENTDEM 1258  
Qy 1259 IDTRIDVTIRIPAGSDTPCLKISHNTFETMEKANWFLRLSLPVTICHNEFIDEAEKARRW 1318  
Db 1259 PDCRIDVTIRIPGADTPPHLKISHNTFETMEKANWFLRLSLPVTICMGEFTSEQEKARRW 1318  
Qy 1319 VEIKROQILMKEA-VEAQM-----PAHIDQIMRSGFTWMDIKGLHYE-DNOEELPSSKM 1371  
Db 1319 DEIKNRQYRLMREABIAAQMOVQTAAHMDHMLKGFNNMDIKGLTRNFDEHADAEADHM 1378  
Qy 1372 KRLSPRPKSGMTGVTIONYNNLQPGOVNGMHRSTSEAWAKYDLGAQGLTDPDKKOK 1431  
Db 1379 MRGNRPKSGLSRNTIT---FETDMSAALDEMRSTST-----VLDMNGLGEEMDDKK-K 1429  
Qy 1432 RGRSPFKFRSGRSSDRAKSRKSTDPDPFDTSEVSPERGARRNPQIKVSAQNRVNG 1491  
Db 1430 RGRSPFKFP-SKSRDQREK-MGARTLDTSLERNTVAHGRNVVQWMTTRAPTFLRNN 1487  
Qy 1492 MNARPSRNLXGSOVLNMMATPDQRKQMTTSLAQSATETVGNBIFDAECLKLNEYFY 1551  
Db 1488 AEIPEPSPV-----POGPKQLSGSLGOQPVETSGDEMFAECLKLNEYFY 1533  
Qy 1552 GVRIVPGODPTHVYIGWVTTQHLHSKDFNQSKVTKSSVIIITDDYDRVVENVNROSQYV 1611  
Db 1534 GVRIFPGODPTHVYIGWVTTQHLHSREFNKNKVRGSIYIBDDYEMAIETIDROSQYV 1593  
Qy 1612 RADELVNEVMAEATAGKASQGMFICSDVTSTGVSFTCEGKDTSFKPMETKLFPAI 1671  
Db 1594 RADELVNEVTTQASGKASQGMFVCGFVDATLGIIRFTCEGKDTSHRWMEPDKLFPAI 1653  
Qy 1672 FVEATSKELIQTIELGRSATSPLSAVLPTSDKHVIPQPPRLKVQCLKPHQWARVPNQS 1731  
Db 1654 FVEATSKELIQTIELGRTPPTLPLSAVLPTSDKHINPQSPPLKVQCLRPHQWARVPNTA 1713  
Qy 1732 LQVHALKUSDTRGWSMLCEDAVSMALHPIBEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791  
Db 1714 LQVHALKSLDVRGWSMLCEDPVSMLALHPIBEDRCIDILEPIEMDKLLSFHAHSHTLYAA 1773  
Qy 1792 LCYQSNVRAAHALCHTVQKOLLYATOSQYMSGSLRQGFYDLILALHLESHATTWEACIN 1851  
Db 1774 LCYQSNVRAAHALCHTVQKOLLYAIRSEYMGSLRQGFYDLILALHLESHATTWEACIN 1833  
Qy 1852 EFVILPLGELKALYBEPDMGHLSRLSLOTESVRFQMKWTDIAESITEISNLSPFYFPLEVA 1911  
Db 1834 EYITPLGAELKELYDEENQHSRLSVLTESVRFQMLRMTETIETPIDQLYSPKPLEVV 1893  
Qy 1912 REFVMOALAEAVETNOVNRDPVGGSENFLPLIKLVDRLLLVGMRRDEDVEKLLIWTN 1971  
Db 1894 RQFVMEALKDAVEINQVNRDPGTWNTNENLFLPLIKLTDRLLLVGLVTDVEDVQRLVMID 1953  
Qy 1972 PETWDSFKEGKDEHRKGLLHMWMAEGAKLQWYLLQHLNDIOLRHRVEALIIAFAHDFV 2031  
Db 1954 PETWQAFREGKDEHRKGLLHMWMAEGAKLQWYLLHHLHYDTQURHRVESIIAASHDFV 2013  
Qy 2032 GDLQTDOLRYTEIKQSDLPSSAAKKTREFRCPPREQNNALISFKHLEEDKENCPCGE 2091

Db 2014 GDLQTDOLRYTEIKQSDLPSSAAKKTKEFRCPPEQMNOILCFKNLEPDQDNCCTGL 2073  
Qy 2092 ELIARMNEFDHDLMAHVSYHALQEPDAAENQEB-PEAKPGFAGKLYNINTVKELEEEAKA 2150  
Db 2074 ELRGLGDHFDLSLMQKVSNALQEPDGVGTAIBEVTGPTTKIYNFINTVKELEEGPKE 2133  
Qy 2151 IEPPPKTPEBKPKVLIQTIIVNWAESQIETPKLVREMFSLLYQVDANGELTRALEKT 2210  
Db 2134 VEPEKKTPEBPVKVLIKTIIVNWAESQIETPKLVREMFSLLYQVDANGELTRALEKT 2193  
Qy 2211 YVINAKTKLDVAEMWVGLSQRALLPVQMSQEEBELMRKRLKLVNHNHTFQHPDLIRVL 2270  
Db 2194 YVINTRADDVAEMWVGLSQRALLPVQMSQEEBELMRKRLKLVNHNATFQHPDLIRIL 2253  
Qy 2271 RVHENVMAVMNTLGRRAQAOQSDAQSPSPVAE--DSKEKDTSHEMVACCRFLCYFRT 2328  
Db 2254 RVHENVMAVMNTLGRRAQAOQSDA-PTQSEVAEGAPSKEDTSHEMVACCRFLCYFRT 2312  
Qy 2329 GRQOKAMFDFHFDLLENSNILLSRPSLRGSTPLDVAYSLSLMENTELALAREHYLEKIA 2388  
Db 2313 GRQOKAMFDFHFDLLENSNILLSRPSLRGSTPLDVAYSLSLMENTELALAREHYLEKIA 2372  
Qy 2389 VYLSRCLQSNSELVEKGYDGLGWDVPEGERYLDFLRCVWVNGESVEENANLVIRLLIR 2448  
Db 2373 VYLSRCLQSNSELVEKGYDGLGWDVPEGERYLDFLRCVWVNGESVEENANLVIRLLIR 2432  
Qy 2449 RPECLGPAALRGEGEGLLAKAIVDANKMSERIADRRKLRJEMEQEGDV--NFSHPLPESDED 2505  
Db 2433 RPECLGPAALRGEGEGLLAKAIVDANKMSERIADRRKLRJEMEQEGDV--NFSHPLPESDED 2491  
Qy 2506 EDYIDTGAAILNFYCTLLVDLLGRCAPDAGVATLAKNESLRARAILRSLVPLEDQGVLSL 2565  
Db 2492 EDYIDTGAAILNFYCTLLVDLLGRCAPDAGVATLAKNESLRARAILRSLVPLEDQGVLSL 2551  
Qy 2566 RFTLNNPAGGERPKSDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLBEAFUPLDRA 2625  
Db 2552 KFTLSQTPAGBEKPKSDMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLBEAFUPLDRT 2611  
Qy 2626 ATMLDRNDGCSMDALSMNRYIGNSILPLLIKHAIFYNEAENYASLLDATLHTVYVLSKN 2685  
Db 2612 ATMLDRNDGCSMDALSMNRYIGNSILPLLIKHAIFYNEAENYASLLDATLHTVYVLSKN 2671  
Qy 2686 RMLTKGOREAVSDFLVALTSAMQPSMLLKLRLKLTVDVSKLSEYTTVALRLTLHYERCA 2745  
Db 2672 RMLTKGOREAVSDFLVALTSAMQPSMLLKLRLKLTVDVSKLSEYTTVALRLTLHYERCA 2731  
Qy 2746 KYGSGTAGOAGFAGASSDEEKRLTMTLFSNIFDSLSKMDYRPELFGKALPCLIAIGCALP 2805  
Db 2732 KYGST-QGQSGYAGASSDEEKRLTMTLFSNIFDSLSKMDYRPELFGKALPCLIAIGCALP 2790  
Qy 2806 PDYLSKNYDDBFYGKEQAAGDLNPOYDPOPIINTSSVALANDLNTIIVQKSEHYHDWA 2865  
Db 2791 PDYLSKNYDDBFYGKEQAAGDLNPOYDPOPIINTSSVALANDLNTIIVQKSEHYHDWA 2848  
Qy 2866 SRKINGWVYGEGBSDSOKTHPRLPKYNMNDYKERYKEPVRESLKALLAIGWSEHSE 2925  
Db 2849 SRLEGGWYGDIRSDNDRKHPRLKPNMSEYERERYPVRECLKGLLAIGWSEHSE 2908  
Qy 2926 VDIPSNRSMRROSKSGRPEI--VTDSATPPDYNPHPDVDMTNLTLSREMNMAERLA 2983  
Db 2909 VEVLNHRGSTRQSK-----PQINEFQNEGSPFNYPHVPDMSNLTLSREMNMAERLA 2963  
Qy 2984 DNAHDIMAKKKEELVTNGGGIHPOLVPYDILLTDEKKEKDRSOFELKYLQYQYKLRH 3043  
Db 2964 ENSHDIWAKKKEELVTNGGGIHPOLVPYDILLTDEKKEKDRSOFELKYLQYQYKLRH 3023  
Qy 3044 PSKAPQSDTEQTTTGTVAIELRPAYSLEKLIQYIDRATINMKLLKPSPTTFSRSSFKTST 3103  
Db 3024 PSKGAIVE-EGGATQAAVELRFSYLSLEKLIQYIDRATINMKLLKPSPTTFSRSSFKTST 3082  
Qy 3104 RDIKFSKAVLPLMEKYFSTHRNYFIATATANNYGAASLKEKEMVAALFCKLASILRR 3163  
Db 3083 RDIKFSKAVLPLMEKYFSTHRNYFIATATANNYGAASLKEKEMVAALFCKLASILRR 3142







Qy 1857 LG-----PELKALYBEPDMGHLSRSLOTES-----VRPQMKTMDIAESI 1895  
Db 117 YGNVIQLHLKSNKYLTVNKRKLPALEKNAMRVTLDEAGNBSGWFIQPFYFKLRSIGDSV 176  
Qy 1896 TEISNLSPYPPLEVAAREFVMOALAEAVETNQVHNRPVGGSENENLFLPLIKLVDRLLLV 1955  
Db 177 -----VIGDKVLPVNPVAGQPLHASSH-----QLVDN---P 204  
Qy 1956 GMMREDEVE-----KLLIMTNPETWDPSPFKBEGKDEHRKG---LLHMKMAEGAKLQMCYLL 2008  
Db 205 GCNEVNSVNCNTSNKIVLFMK---W-----SDNKDDILKGGDVVRLFAHEQEKFLTCD-- 254  
Qy 2009 QHLNDIQLRHRVEAIIAFAHDFVGDLOTQDLRRYTEIKOSDLPASAANKTREPCPRE 2068  
Db 255 -----EHRKK-----QHVFL-----RTTGRQS--ATSATSSKALWEVEVVQHD 290  
Qy 2069 -----QMNAILSFKHLEEDKENCPCGEBELIARMNEFHTLMAHVSLSHALQPDAAEN 2121  
Db 291 PCRGAGYWNLSLFRFKHL-----ATGHVLAAEV-----DPD----- 321  
Qy 2122 QEPEAKPGAFOGLYNIINTVKELBEEAKAIBEPKKTPEE-----KFRKVLIIQITVN 2173  
Db 322 -----FEEE--CLEFQSPVDPDQDASRLRNAQEKWVYSLVS 357  
Qy 2174 WAESQIET-----PKLVREMFSLVRQYDAVGELIRALEKTYVINAKTKLDVAE----- 2223  
Db 358 VPEGNDISSIFELDPFTTLRGDGLSVPR--NSYVRLHRLCTNWTWVHSTNIPIDKEEEKPVM 415  
Qy 2224 MWVGLSOIR-----ALLPVQMSQEBE-----ELMRKRLWK 2253  
Db 416 LKIGTSPVKEDKEAFAIVPVSFAVRDLDPANDASKVLGSIAGKLEKGTITONERSVTX 475  
Qy 2254 LVNNHTFF-----QHPDLIRV-----LRVHENVMVMMNTLGRRAQAQSAQP 2296  
Db 476 LLEDIAVFTVGTNSQDVLVWFVSKPNRRQKLMREQNILKQIFKLLQAPFTDCGDG-- 533  
Qy 2297 SSQPAEDSKEDTSHENWVACCFLYFC-----RTGRONKAMFDPHFLLENSNILL 2351  
Db 534 ---PMLREELGQDRHAPPFRHICR--LCYRVLRHSQDQYRKNOEYIAKQFGFMQK----- 583  
Qy 2352 SRPSLGRSTPLDVAYSSLMENLALAREHYLEKIAVYLSRCGLQNSLSEVEXGYPDLG 2411  
Db 584 -----QIGYDVLAETITAL-----LHNNRKLLEKHITAAE 614  
Qy 2412 WDPV-----EGERYLDPLFR--FCVWNGESV-----EENANLVI---RLIIR 2448  
Db 615 IDTFVSLVRKNRPREPRFLDYLSDLCVSMN--KSIPVTQELICKAVLENPTNADILITKLVL 673  
Qy 2449 RPECLGPALRGEGLLKAIYDANKM-----SERIADRRKLREMEQEGDVNFSGHPLPES 2502  
Db 674 RPEFEG--VSSTGENALEAGEDEEVWLFWRDSNKERSKSVRELAQDAKEG-----Q 724  
Qy 2503 DEDEDYIDTGAAILNFYCTL-----VDLLGRCAPDAGVIALGKNESSLR 2545  
Db 725 KEDRDVLSYRYQNLNPFARMCLDRQYLAINEISQLDVLILRCMSDENL-----PYDLR 779  
Qy 2546 A---RAILRSILVPLEDQGVLSLRLFTLNNPAAGEERPKSDMPGSLIIPGHKQSVGLFLERV 2602  
Db 780 ASFCRLMLMHVDRDPQOVTPVKYA-----RLWSEIPSEIADDDYSSGASKD-- 828  
Qy 2603 YGIETOELFYKLE--EAFPLDPLRAATMLDRNDGCESDMALSMRYTGNSTILPLLIKAY 2660  
Db 829 ---BIKERFACTMEFVEEYLRDV--VCORFPFSDKEKNKLTPEVVNLAARNLI-----YFG 878  
Qy 2661 FYNEAENYASILLDAT-----LHTVYRLSKNRMLTKGOREAVSDFLVALTSAMQP 2709  
Db 879 FY-----NFSDLRLTKILLAILDCHVTITIPISK---MAKGE----- 915  
Qy 2710 SMLLKLRKLTVDSKLSYTTVAL-----BLTLHYERCAYKYYSGTGAGQAGF---A 2760  
Db 916 -----NKGNDVLEKLSNNMRSIHGVBELMTQVVLRGGFLPMTPMAAAPEGNVKQA 968  
Qy 2761 SSDEEKRLTMMFLSNIFDLSL-----KMDYEPFELFGKALPCLIIAIGCALPDPYISKNYD 2815

Db 969 EPEKEDIMWMDTKLKIEILQFILNVRLDYR-----ISCLLCI-----FK 1008  
Qy 2816 DEFYGKEQAAGDLDNPQYDQDPQINTSSVALNNDLNTIVQKSEHYHDAMASRKIENGWY 2875  
Db 1009 REF-----DESNSQ-----TSETSSGNSQ----- 1028  
Qy 2876 GEGMSDSOKTHPLKPVNMLNDYEKERYKEPVRESLKALLAIGWSVSEHSEVDIPSNRRSS 2935  
Db 1029 -EG-----PSNVPGALDFEHIEQA--EGIPGGRKVYFHEENTPLDLDDH----- 1070  
Qy 2936 MRQSKSGGRPEIIVTDSATPFDPYNNPDPVDMTNLTLSREMNMAERLADNAHDIAWAKCK 2995  
Db 1071 -----GGRTFLRVLLHLTHDYPP-----LVSGALQLLFRHFSQRQEVLQAFQV 1115  
Qy 2996 EELVTNGGGIHPOLVPYDLTLTDEKKKDRERSQEFKLYQYQGYKJLHRPSK-----APQS 3050  
Db 1116 QLLVTS-----QVDVNYKQIQDLDQLRSIVEKSELWYKGGQPDETMDGASGEN 1165  
Qy 3051 DTEQTTTGAIELRPAYSLLEKLIQYIDRATINNKLLKPSTTFSSRRSSFTKTRDIKFFS 3110  
Db 1166 EHKTEEG-----NNKPOKHEST-----SSY----- 1186  
Qy 3111 KAVLPLMEKYFSTHRNYFIATATNNTNNGAASLKEKEMVAALFCKLASLRLSRLAFCPD 3170  
Db 1187 -----NVRVV-----KEIL----- 1195  
Qy 3171 VRITVRCLOVLVGIDAKSLVKNCPEPIRFSMTLTFNNVADDVGHITMNLQDGKYAHLRG 3230  
Db 1196 IRLSKLCVQ-----ESASVRKS-----RKQORLLRNM-----G 1224  
Qy 3231 THLKTSTSLGYINGVLLPILTAKEFDHLANCEYGADLLLDLDEIOVASYKMLGSLYALGTDS 3290  
Db 1225 AH-----AVVLELQIPI-----EKAEDTKQIMRLAHEFLQNF----- 1259  
Qy 3291 LTHDRKYLKTEIBRHKPALGSCGLGAFSSTPFVAFLEPHLNKNQFSLNLIADHSLEAQD 3350  
Db 1260 -----CAGNQNQ---ALLHKHINLFLNPGILEAVTMQHI--- 1291  
Qy 3351 IMQMBQCMPTLETILGEVDQFVESDKTYNEAPHIIDVPLLCLSYLPFWWAQPDNVTP 3410  
Db 1292 FMNPFQCSBNERV--VQHVV-----HCIE----- 1315  
Qy 3411 TCGNHYTMVTAEHMQLKNVLIKNIGNENAPMWTIATVTOQIIINSSEBLL--- 3466  
Db 1316 THGRNQVYI--KFLQITIVKAEGRFIKK-----CODMMAELVNSGEDVLVFN 1361  
Qy 3467 -RDSFLPLAERVRKRTDNM-----PHKEESLRGFIKSDTDDTSQVESIQIEDWOLL 3516  
Db 1362 DRASFQTLIQMBSERDMDENSPLMYHIHLVELL-----AVCTEGKNVYTEIKCNLLP 1416  
Qy 3517 VRDIYSPY-----PLLIKYVDLQRNHWLRNNVPEABELY--NHVAEIFNIMSKSQYFL 3567  
Db 1417 LDDIVRVVTHEDCTIPEVKIAYINF-LNHCVYDTEVENKEIYTSNHHMKLF----- 1465  
Qy 3568 KESQNFISANEIDNNVLMPTATRTATRVAVTDGTPQGCGKKKKKHKRDKRKD--DKEVOASL 3626  
Db 1466 ---ENFL---VD-----ICRACNNTSD-----RGHADSILEKYVTEIWMSI 1500  
Qy 3627 MV-----ACLKRLLPVGLNLPAGREQELVQCHDKRFLKKNSEQDY-----AE 3668  
Db 1501 VTTFFSSPFSQDSTTLTROQPFVQLLQGVFR--VYHC--NWLMPQSKASVESICIRVLSD 1556  
Qy 3669 FAKTQ-LTLPDKID-----PADEMSWHYLYSKLGSKSKSNIT----- 3705  
Db 1557 VAKSRAIAIPVDLDSQVNNLFLKSHSIVQKTAMNWR--LSARNAARDSDVLASRDYRNI 1614  
Qy 3706 VETAENKAKIIDTVERIV-AMSKVLFGHLHMDHPQOMKNVRSVSIQKRAVIACFR 3764  
Db 1615 IERLQDIVSALEDRLRPLVQAEISVL--VDVLRHPELL-----PFENTDARK--CES 1663  
Qy 3765 QTSIHLSPRH-----RACNIFARTYELWLEBENITGQEYMIEDLTQSFEDAEL-- 3812

Db 1664 GGFICKLIKHTKQLLENEEKLCIKVLOTLEMMTKDRGYGEKLSID---ELDNAELPP 1720  
Qy 3813 --KSDVVEEGKPDPLTQVTFPCRGMATERSGALQSDPLVMSYAHIIAKSCGEBE-- 3868  
Db 1721 APDSENATEELPSPPLQLED-----HKGEALRQVLVNRYYGNV--RPSGRRESLT 1771  
Qy 3869 -----EGGSEEGGGEAEAEDEGRASIHEQEMEKOKLPHQARLADRGAEMVL-LH 3920  
Db 1772 SFGNGPLSAGGPKPGGG---GGSGSSMSRSGEMSLAEV---QCHLKEGASNLVIDLI 1825  
Qy 3921 ISASGKLSEVMWKTLQIGISILRCGNIDIQMGLNHL-KKKOVGFF----- 3967  
Db 1826 MNASS---DRVPHESIALLAILEGNTTIQHSFPCRLTEDKSKKFFKVFYDRMKVAQQ 1882  
Qy 3968 ---TSIAGLWNSCVLDLDAFERNTKAEGL----- 3994  
Db 1893 EIKATVNTSDLGNNKKDDVDVRDAPSRKKAKEFTTQITEVRDQLLEASAAATRKATTT 1942  
Qy 3995 -----GVGLEGAAGEKNMHAETCA-----LFRFTQLTCEGHNDLQNYL 4035  
Db 1943 FRREADPDHYQPGSGTQ-ATADKAKDDLEMSAVITIMQPIILRFLQLLCEHNRDLQNFL 2001  
Qy 4036 RTQAGNTTNNVVICTVYLLRLQBS-----IMDFYWHYSKELIDPAGKANFFKAGV 4089  
Db 2002 RCQ-NNKTNYNLVCTLOFLDCICGSTTGGGLGLGLYINE-----KNVAL 2045  
Qy 4090 ASOVENTLTVLOQCTQOQALAHSLWDVGGFLFLFSHMQDKLSKHSQVDLLKELL 4149  
Db 2046 INQTLSTLEYCGPCHENQNCIA-----THESNGIDIITIAL- 2082  
Qy 4150 NLOKDMIPMLSLMGVNVGTIGQVMDTLVE-SASNVLEILKYDFMFLKLKDLTSSAS 4208  
Db 2083 -ILNDINP-----LGKRMDLVLELAKNAKSKLL-----LAIMESHDSN 2122  
Qy 4209 FOEIDANNNGWVLPKDFKEMEQKSYTPEETIEFLACETNHDGKLDYIGFCDFRHPA 4268  
Db 2123 ABERILYN---MRPKELVEVI-KKAYMQGEVEF-----EDGENCE-----DGAASP- 2163  
Qy 4269 KEIGNLAVLLTNSEHPNEPRLARFLETAGSV-----LNYPEFLGRIETMGSKIE 4323  
Db 2164 RVNGHNIYILAHQLARH---NKELOSMLKPGQVGDDEALEFYAKHTAQIETVRLDRME 2220  
Qy 4324 RYVFIEKESNIBQWEKPOI-----KESKRAFFSYIVTEGGDK-EKLEAFVNPCEDAIFEM 4377  
Db 2221 QIVFPV-----PSICEFLTRESKLRIYTT--TERDEQSGKINDFFLRSEDLFNM 2268  
Qy 4378 THASGLMAASEBSVGGTKNREASYMYMGDDDDERAGKDPFRRLGLOSVDGVATAFSSLS 4437  
Db 2269 NWQKKLRA-----QPVLYWCARNMSFW-- 2290  
Qy 4438 SNIKAKIADMOQMPAELAVGFFKMFYLYLGYGVLVVRYIRGVLLGLMRGPOTDEP 4497  
Db 2291 SSIISFNLAIVMLNLLVA-----FFYPFKGVGGTL----- 2319  
Qy 4498 PPEPTEEEKIGQLRHLLATQSSRHLPALPPADDTQGMQVSFAFLDITKEDNGQIQVKPH 4557  
Db 2320 -----EPH 2322  
Qy 4558 ESPSTSTPSGSEAEVSPDESADHTEEQRPSPSLIDLLGGEQAKQAQERMEAAQAQAAM 4617  
Db 2323 WS----- 2324  
Qy 4618 SAIEAESKAVOGPAPALSQVDLSQYTRAVSFLARNFYNNKYVALVLAFCINFLVLY 4677  
Db 2325 -----GLLTWAMLISLAIVIAL--- 2341  
Qy 4678 KYSTLDGEGGSGLDIIAGGSGGAGSGSGSGESGEDDDDALEVHIDEDEFYMEH 4737  
Db 2342 -----KPHGIRALIA----- 2352  
Qy 4738 VIKMAAVLHSIVSLAI-----LIGYVHLKVP LAIFKREKEIARKLEFDGLYIAEQPEDDD 4792  
Db 2353 -----STILRLIFSVGLQPTFLFLGAFN-----VCNKLIIF----- 2382

Qy 4793 LKSHWDKLIVASGFPVNYMDKFVKKVRAKYSYDFDSDISNMLGMEKTSFSAQEBEGS 4852  
Db 2383 ----- 2382  
Qy 4853 KGLHYIINDIRYQVWKAGVTITDNSFLYSIWTYFSVMGNF--NNPFAAHLDDVAVGF 4911  
Db 2383 --LMSFVGNCGTFFRGYRA--MWLDVEFLHLLYLVICAMGLFVHEFFYSLLFLDLVYRE 2438  
Qy 4912 KTLATILQSVTHNGKQVLVLTVMLLTIIVYIVTVAENFFRKFFV----- 4955  
Db 2439 ETLNVIKSVTRNGRSIILTAVALIILVYLSIVGYLFFKDDFILEVDRLNETAVPTG 2498  
Qy 4956 -----QEEDEVNVRNCHDMLTCTFVFNLYKQVR 4982  
Db 2499 ESLASEFLFSDVCRVSEGENCSSPAPREELVPAEETEQDKEHTCETLLMCIVTVLSHGLR 2558  
Qy 4983 AGGIGIGLEPPDGDGDS-EVYRIIFDISFFFIIVILLAILOGLIIDAFAELRDQLESVK 5041  
Db 2559 SGGGVGDVLRKPSKEEPLFAARVYDILLFFFMVIIIVLNLIIFGVIIIDTFADLRSEKQKE 2618  
Qy 5042 EDMESNCFICGINXDYFDKVPHGFDTHVQREHNLANTYMFELMHLINKPDTXTGQETVW 5101  
Db 2619 EILKTCFICGLERDKFNDKTVTFEEHKEEHNMMWVLCFIVLVKVDSTETYGESYVA 2678  
Qy 5102 NMYTORCWDFPP 5113  
Db 2679 EMIKERNLDWFP 2690

## RESULT 2

US-10-505-928-784  
; Sequence 784, Application US/10505928  
; Publication No. US20060089532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
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; SEQ ID NO 784  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-505-928-784

Query Match 2.2%; Score 601.5; DB 6; Length 2671;  
Best Local Similarity 17.4%; Pred. No. 9.2e-28;  
Matches 625; Conservative 475; Mismatches 1060; Indels 1427; Gaps 149;

Qy 1932 DPVGSSENFLPLIKLVDRLLLVGMWRDEVEKLLIMTNPETWDPSPDEKGGDEHRKGL 1991  
Db 39 EPAAGDLDN---PPKKFRDCLFKVCPMRYSAQK-----QYWKAKQTKQDEKIADV 88  
Qy 1992 LHMKAQAGAKIOMCYLIQHLND-----IQRH-----RVEAII 2024  
Db 89 LLQKLQHAQAQME-----QKQNDTENKKVHGDVWYKGVSVIQLLHMKSNKYLTWNKRLPAL 143  
Qy 2025 -----AFHDF-----VGD---LQTDLRRYTEIKOSDLP 2052  
Db 144 EKNAMRVTLDTAGNEGSLFIQPFWKLRSGDNVVGDKVILNPNVAGQPLHASNYEUSD 203  
Qy 2053 AVAAKKTREPPCPPEOMNAILSFK-HLEE-----EDKENCPCGEELIARN 2098  
Db 204 NAGKEVNSVNCNTSKINLFMQFRDLHEEVKGGDVVRLFHAGQEKELTLC-DEYKGLQ 262  
Qy 2099 EFHDTLM-----AHVSLHALQEPDAAENQEPKPAFGKLYNIINTVKELEE-EAKAIE 2152  
Db 263 VFLRTTLRQSATSATSSNALWEVHVHDPCKRGAGHNGLYRF-----KHLATGNYLAAE 318

Qy 2153 EPP-----KKTPEEKFRKVLQIOTVNWAEBSQIE-TPKLVREMP 2190  
Db 319 ENPSYKGDASDPKAAGMGAOGRTRRNAGEKIKYCLVAVPHGNDIASLFDLPTTKTD 378  
Qy 2191 SLLVRQYDVGELIRALEKTVINAKTKLDAVE-----MMVGL 2228  
Db 379 SFVR--NSYVRLRHLCNTNTWQSTNVPIDIEERPIRLMLGTCTKEDKEAFAIVSPV 436  
Qy 2229 SQIRALLPVQMSQEBEELMRKRLKLVNNHTFFQHPDLIRLVHE----- 2274  
Db 437 SEIRDL---DFANDASSMLASAVEKL--NEGFSQNDRRFVIQLLEDLVPFVSDVPPNGQ 491  
Qy 2275 NVMAVMNTLGRRAQASDAQSSQPV-----AEDSKEKDTSHE- 2313  
Db 492 NVLDIMVTKPNRQRKLMREQNILKQVGLKVPFREKGGGGLVRLEELSQQKNAPYQH 551  
Qy 2314 MVVACCRFLCYFCRTGRQONKAMDFHDFLLENSILLRSLSLSTPLDVAVSSLMEN 2373  
Db 552 MFLCYRVLRSQEDYRKNQBIHAKQF-----GMMQSQIGYDILAEDT 594  
Qy 2374 ELALALREH-YLEKIAVYLSRCGLQNSSELVEKGYPDLGMDPVEGERYLDFLR-FCVMVN 2431  
Db 595 ITALLHNRKLEK--HITKTEVETFSVLVRKN-----REPRFLDVLSDLCV- 639  
Qy 2432 GESVEENANULVIRLLIRPECLGPAALGEGGLLKAIVDANKMSERADRKLREMEQEG 2491  
Db 640 -----SNHI-----AIPVTQELICKCVLDPK--NSDILIRTEL- 671  
Qy 2492 DVNFSHPLEPSEDEDEYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNSLRARAILR 2551  
Db 672 -----PVKEMAQSHESYLSIBYSEEVWLTWD-----KNEHHEKSV-R 709  
Qy 2552 SLVPLEDQGLVLSRFTLNNPAAEERPKSDMPGLIPGHKQSVGLF-----LERYV- 2603  
Db 710 QL-----AQEARAGNAHDENVLSYRYQLKLFARMLCDRQYLAD 749  
Qy 2604 GIETQ---ELPYKLEBAFLP-DLRAATMLDRNGCSDMAISNMVYIGNSILPLLKHA 2659  
Db 750 EISQQLGVDLILFLCMADEMLPDLRAS-CHMLHLHVHVDROPQELVTP--VKFA 800  
Qy 2660 FYFYE-----AENYASILLDATLTVYVLSKNRMLTKQREAVSDFVALTSAMQPSMLL 2713  
Db 801 RLWTEIPTAITIKDYDGNLNASRDDKKNKFANTW-----EFVEDLNNVVSEAVP-FAN 853  
Qy 2714 KLLRKLTVDSKLSSEYTTVALRLTLHYERCAKYTGSTGAGQAGFAGASSDEEKLTWMLF 2773  
Db 854 EEKKNLTFEV-----VSLAHNLI-----YFGF-----YFSSELLRLTRL- 888  
Qy 2774 SNIFDSLSKMDYEPFLFGKALPCLIAIGCALPPDYSLSKNVDDEFYKQEQAGDLNPOY 2833  
Db 889 -----LGIIDCVQGP-AMLQAYEDP-GGKN----- 912  
Qy 2834 DPQINTSSVALNNDLNTIV-----QKFSHYHDAMAS-----RKIENGWYVGEQMSD 2881  
Db 913 -----VRRSIOGVGHMMSTWLSRKQSVFSPSLSAGASAEPLDRSKFEEN-----ED 961  
Qy 2882 SQKTHPLRKPYNMLN-----DYE-----KERYKE-----PVRESLKA 2913  
Db 962 IVWETKLIKILEILOFILNVLDYRISVLLSVFKFEVFPMDQSGADGTAPAFDSTA 1021  
Qy 2914 LLAIGWSVEHSEVDPISNNRSMRRQSKSGRPPETVDSATPPDYNP----- 2961  
Db 1022 NNMLDRIGEQAEMFGVGKTSMLLEVDDGGRMFLRVLHLTHDYAPLVSQALQLLFXH 1081  
Qy 2962 -----HPVDMTNLTLRE-----MOMAEERLADNAHDITWAKK---KE 2996  
Db 1082 FSQROEAMHTPKQVOLLISAQDVENYKIVKSELDRRLTMWEK-----SELWVDKKGSGK 1136  
Qy 2997 ELVTNGGIGHQLVPYDLTLTDEKKKDRERSQEFKVLQYQYKHLRPSKAPQSDTBQTT 3056  
Db 1137 EEVEAG-----TAKD-KKERPTDEE-----GF-LHPGGE-KSENYQIV 1172

Qy 3057 TGVAIELRPAYSLE-----KLIQVIDRATINMKLLKPBSTTFSSRSSPKTSTRODKFF 3109  
Db 1173 KGLERLNKMGVGEQMRKKQQLDLKNMDAHKVMLOLLQIP-----Y 1214  
Qy 3110 SKAVLPLMEKYFSTHRNYFIATATNNVGAASLKEKEMVAALFCKLASLLRRLAAGP 3169  
Db 1215 DKGDAMMEILRYTHQ--FLQKFCAGNPGQA-----LLHKHLHLF-- 1253  
Qy 3170 DVRIITVRCLOVLKVIDAKSLVKNCPEFRTSMLTFFNN--VADDVCHTITNLODQKYAH 3227  
Db 1254 ---LTPGLLEA-----ETMQHIFLNNYQLCSEISEPVLO---HFVH 1288  
Qy 3228 LRGTHLKTSLSLGVINGVLLPILTAKFHDHLANCEYGADLLDEIQVASYKMLGSLYALGT 3287  
Db 1289 LLATHGRHVOYDFLH--TVIKAGKYVKCQ--DMIMTELTA-----GD 1330  
Qy 3288 D-----ASLTHDRKYLKTE---IERHKPALGSCLGAFSFTPPVAFLEPHLNKHNQFS 3336  
Db 1331 DVVVFYNDKASLAHLDDMMKAARDGVEDHSPLM-----YHIS 1367  
Qy 3337 LMNRIADHSLAEADIMQKMB-QCMPTLETILGEVDQFVESDKTYNEAPHIIDVVLPLCS 3395  
Db 1368 LVDLLA-ACAEKGNVYTEIKCTSLVPLEDVSVV-----THE-----DCITEYKMA 1412  
Qy 3396 YLPFWAQQGPDNVTPTGGNHVTMTVAEHMQLKNVLKLIKIGNENAPMTTRIATYQ 3455  
Db 1413 YVNF-----VNHCVYDTEVEM-----KEIYTSNH1W- 1438  
Qy 3456 QIIINSSEELRDSFLPLAERVVRKTDNMFPKBEESLARGFIKSDTDDTSQVESQIQEDWQL 3515  
Db 1439 -----TLFENFTLDMARVCSKR-----EKRVADE- 1461  
Qy 3516 LVREDIYFVPLLLIKYVDLQRNHWLRNNVPABEELYNHVAEIFNWSQVFLKEEQNFIS 3575  
Db 1462 -----PTLEKYV-----LSVLDITINAFESSPF-----SENST 1490  
Qy 3576 ANEIDNNVLMPTATRVTAVTGTPQGGGKKKKHDKKRDKEVQASLWVACLKRL 3635  
Db 1491 LQTHQPVVOLLOSTTRLECP-----WLOQQHGS-----VEACITLA 1530  
Qy 3636 PVGLNLPAGREQEVLVHCKDRFLKQMS-----BQDVAEFAKTQTLTPDKIDPADEMSQW 3690  
Db 1531 MVAKGRALLPMDLDAHISMLSSGASCAAAQARNASSYKATTPRAFPVPTANQ--WDY 1588  
Qy 3691 YLYSKLGSKSKSNITVETAEKAKIIDDTVERIV--AMSKVLFGHMDHPHQMSKNVYR 3748  
Db 1589 -----KNI-IEKLODIIITALEERLKLPLVQAELSVLVDLH-----WP 1624  
Qy 3749 SVVSIQRKRAVIACFRQTSLSLSLPRH-----RACNIFARTYVELWLEENIG- 3795  
Db 1625 ELFLPGESEAYQCEGGFLSKLIQHTKDLMESEKLCIKVLRTLOQMLVKTKYGDRCN 1684  
Qy 3796 --QEVMIEDITQSFDAELKSDVBEQKPDPL-TOLVTTFCRGAMTERSGALQEDPLY 3852  
Db 1685 QLRKMLLQNYLN-----RKS-TSRGDLPPDPIGTGL-----DP- 1716  
Qy 3853 MSVAHIIAKSCGEBEEBEGGEEGGEAEAEDEGRASIEHEQMEKOKLJLHQARLADRG 3912  
Db 1717 -DMSAATAQC-----RDKKEG 1732  
Qy 3913 VAEWVLLHLSASKGLPSEVMYMKTLQGLISILRGNDIDQMGLN-HLKDKKDVGF- 3967  
Db 1733 ATKLVCDLITSTKN--EKIPQESIGLAHLDOGNTEIQKSFNLNMSDKSKSRFFKVLH 1790  
Qy 3968 -----TSIAGLNNSCSVL---DLDAFERNTKAEGLGVGLEGAAGEKN- 4007  
Db 1791 DRMKRAQOETKSTVAVNMNDLGSQPHEDREPVDPTTKGRVASFSIPGSSRYSLSGLR 1850  
Qy 4008 -HDAE-----FTCALFRFIQLTCEGHNDWQNYLRTQAGNTTIVNVICTVD 4053  
Db 1851 GHEVSERVQSSEMGTSLVIMQPIRLFQLLCENNRDLQNLFCQ--NKNYNLNVLCETLQ 1909  
Qy 4054 YLLRLQES-----IMDFYWHYSSKELIDPAGKANFPKAGVASQVNTLITVIGQPCQT 4107









Qy	2502	SDEDEDYIDTGAAILNFYCTLVLDLGRCAPDAGVIALGRK-ESLRARAILRSVLPLEDLQ	2560
Db	859	QELQEEY- ---ACLLKVKDDLED- ---SKNQBLEYKSKLKALNEELHLQ	900
Qy	2561	GVLSLRTFLNPAAGBERPKSDMPGSLIPGHKQSVGLFLE--RVYGIETOELFYKLLSEA	2618
Db	901	RI- ---NPTTVK- ---MKSVFDEDKTFVAETLEMGEVVEKDTTLMELMEK-LEVT	945
Qy	2619	FLPDLRAATMLDRNDGCESDWALSMNR- ---YIGNSI- ---LPLLI	2656
Db	946	KREKLELSQRLL- ---SLSBQLKQKHGEISFLNEEVKSLKQEKQVSLRCRELEIIL	998
Qy	2657	KHAYFYNEAEN- ---YASLLDATL- ---HTVYRLSKN- ---R	2686
Db	999	NH- ---NRAENVQSCDQVQSVSLLDGVVTMTSRGAEGSVKVNKSVFGESKIMVEDKVSE	1054
Qy	2687	MLTKG- ---QREAVSDFLVALTS- ---ANQPSMLLKLRKLTVDSVSKLSEYTTVALRL	2737
Db	1055	NMTVGEESKOEQLTLDLHPVSKTKESSURATOPSENDKQLQELANVLKSEQND- ---LRLQ	1109
Qy	2738	TLHYERCAKYVSGTAGQAGFAGASSDEEKLTMWLFNSNIPDSLSKMDYBEPelfcKALPCL	2797
Db	1110	MEARQICLSLVSYTHVDQVEYMEKDKKALCSLKEELIFAQEBKIK- ---	1156
Qy	2798	IAIGCALPPDYSISKNYDDFYG-KEQAAGDLNPOYDPOINTSVVALND- ---LNTI	2852
Db	1157	---ELOKIHOLELQTMKTQETGDEGKPLH-LLIGKLQAVASEGCSFYLOTL	1203
Qy	2853	VQKPEHYHDWA- ---SRKIENGWYVEGWSDSOKTHPLKPKYNMLNDEKERYKE- ---	2905
Db	1204	CSVLGEYITPALKCEVNAEDKENSQDY- ---ISENEDPELDQYR- ---YEVQDFQENMH	1254
Qy	2906	---PVRESLKALIAI- ---GWSVEHSEVDIPSNRNRSMRQSKSGGRPE	2948
Db	1255	TLLNKVTEYNKULLVLOTRLSKIWGQOTGWMKLEFGEENLPKEBTEFLSIHQ- ---	1307
Qy	2949	IVTDSATPPDYNHPHVDWMTLTSRENONMAERLADNAHDIAWKKKKEELVTNGGHHQ	3008
Db	1308	---MTNL- ---EDIDNVHKS- ---	1321
Qy	3009	LVPYDLTLTDEKKDRERSOFLKLOYQGYKLRHPKAPQSDTEQTTTGVAIELRPAYS	3068
Db	1322	---LSSLODLEKTKLEBQVQE- ---LESLSISOQLQKETEQNYEAIH- ---	1363
Qy	3069	LLEKLIQYIDRATINMKLLXPSTTFSRRRSFKTS- ---TRDIKFFSKAVLPLME	3118
Db	1364	CLQRLQAVSESTVPPSLPVDVSVITESDAQRTWPGSCVKKNIDGTIEFSGE- ---	1416
Qy	3119	KYFSTHRYNIAVATATNNVGAASLKEKEMVAALFCKLASLLSRLAAGFDVVRITVCL	3178
Db	1417	---FGVKEETNIV- ---KLEBKQYOEQLEEEVAKVIVSMSTAFQAQOTEL- ---	1458
Qy	3179	QVLVKGIDAKSLVKNCEPFI RTSMLTFPNNVADDVGHTIMNLQDGKVAHLRGTHLKTSTS	3238
Db	1459	---SRISGGKE- ---NTASSKQAH- ---	1475
Qy	3239	LGYINGVLLPILTAKFDHLANCE- ---YGADLLLDEIQVASYKMLGSLYALGTDASLTHD	3294
Db	1476	---AVCQOEQHYFNEMLKSQDOI- ---GFQTFPTVD	1504
Qy	3295	KYLUKTEIERHKPALGSCLGAFSFTFPVAFLEPHLNKHNQFSLNRIADHSL- EAQDIMQ	3353
Db	1505	VKFX- ---BEFKP- ---LSKELGHEGKBEILLNSNDPHIDPESKO- ---	1540
Qy	3354	KMEOCMPTLETILGEVDOFVESDKTYNEAAPHIIDVWLLPLLCYLPFFWAGQPNVTPTGG	3413
Db	1541	---CVLTIS- ---BEMFSKDTFVIRQSHIDEI- ---SVSSMDA	1573
Qy	3414	NHVTMTVAEHNQLLNKVLKLIKIGNENAPWMTRIATYTOQIIINSSSELLADSLPL	3473
Db	1574	SROJLMNEEQLEDNRQ- ---ELVRQYBHQQATELLRQAHNRQMRQERODEQEQEETIKRL	1630

Qy	3474	AERVURKT	----	DWPHKEE	----	SLRGFIK	----	SSP	----	DDTS	3500
Db	1631	NROLQASSIDNENLVSRERVLLEEALQULSLAGREKLCCELRNSSTQOTONGENQO	1690								
Qy	3504	QVESQIQEDQWL	----	LVRDIYS	----	FYPLLKIYVDLQRNHLWRNNVPE	3545				
Db	1691	EVEEQTFKEKELDRKPEDVPPEILSERNYALQKANNRLKILLEV	1742								
Qy	3546	ABEYLNHVAIFNPKWSQYFLKEEQNFISANEIDNMVLIPTATRRVTAVTD-GTPQGG	3604								
Db	1743	EETIGRHVLGILDRSSKSQ	----	SSASLIWRSEAE	----	ASVKSCVHEBHTRVTDDESIPSYS	1796				
Qy	3605	GKXKKKHRRDKRDKXEVQASLMVACLKRLPVLNLFAGRE	----	QEL	----	VOH	3652				
Db	1797	GSDMPRNDINWASKVTBEGTELS	----	QRLVRSG	----	FAGTETHPDNEEELMLNMISSLQA	1849				
Qy	3653	CKORFLKMKSEQ	----	DVAEFATOL	----	TLDPKIDPADBSMQHYLYSLGSKSKSNIT	3705				
Db	1850	AVSKLLBAISETSQUEHAKVTQTELMWRESFROKQEATESLKQEEELRERLHESRAREQ	1909								
Qy	3706	VETAENKAK-IIDDTVERIVAMSKVFLGFLHMIDHPQOMSKNVYSRVVISIQRKRAVIACFR	3764								
Db	1910	LAVELSKAEGVIDG	----	YADEKTLFER	----	QIQEKTDIIDRLLE	1946				
Qy	3765	QTSLSHSLPRHRACNIFARTYYELWLBENITGOEVM	----	EDLTOSFE	3808						
Db	1947	QELLCASNR	----	LQEEAEQOQIQEERELLSRQKEAMKAPGVPQOOLLOETE	1996						
Qy	3809	DAELKKSDDVVEEGEKDPPLTQLVTFPCRGAWTERSALQSDPLYMSYAHIIAKSCGEEEE	3868								
Db	1997	KJMKKELEVOCQAEK	----	VRDLOQKQVKALEID	----	2026					
Qy	3869	EGGEEBEGGAEAEDEGRASI	----	HEQEMEQ	----	KLLFHQA	----	RLADRGVAEM	3916		
Db	2027	----	VEEQSRFTELEQEKYTELMDLRQONQALEKQLEKXKFLDEQAIADREHERDVFQ	2082							
Qy	3917	VLLHISASKGLPSEMWKTLQLGISILRGNNIDIQMGMLNHLKDKDVGFVFTSIAGLMNS	3976								
Db	2083	EIOKL	----	EQQLKVVPFQPISEHOTREVEQ	----	LANHLKEKT	----	KCSELLLS	2128		
Qy	3977	CSVLIDLDAPRNYKAEGLV	----	GLEGA	----	AGEKNMHDAEFTCALPRFIQLTCEGHNLD	4030				
Db	2129	KEQLORDIQERNEEIEKLEFRVRELEQALLVBERKHFGAVEAKPELSLEVQLOQNERDAID	2188								
Qy	4031	WONYLRTOAGNTTNNVVICTVDYLLRLQBSIMDFYMHYSSKELIDPAGKANFFKAIGVA	4090								
Db	2189	RKE	----	KEITNLEQLQEQF	----	----	----	----	R	2205	
Qy	4091	SOVENTLITEVIQGPCTONQOALAHSLMDAVGGFLFLFSHMQKLSKHSSQV	----	DLLKE	4147						
Db	2206	EELKNKEEVOQ	----	----	----	LHWQLEIQKSESTFRLQLEQE	2239				
Qy	4148	LLNLQKDMIPMULSMLEGNVNGTIGQMVDTLVESASNVVELILKYFDMFLKLDLTSSA	4207								
Db	2240	NKLFKDPMEKLGALIKESDAM	----	STQDOHVLFGKFAQIIQEKV	----	2281					
Qy	4208	SFOEIDANNQGWLPKDFKEKMEQKSYTPE	----	----	----	EIEBFLLA	----	CCE	4248		
Db	2282	----	EIDOLNQ	----	VTKLOOLKITTDNKVIEKNEILRDLETOIECLMSDQBCVK	2331					
Qy	4249	TNHDGKLDYIG-FCDRPHEPAKEIGNFNAVLLTNLSH	----	----	----	MPNEPRLARFL	4296				
Db	2332	RNREEIEQLNEVIEKIQOELANIGOKTSMNAHSLSEADSLKHQLDWVIAEKLALBQQV	2391								
Qy	4297	ETAGSVLNYEPFPLGRITIEINGGSKRIBRVVFEIKESNIEQWEKPO-IKESKRAFFYSIVT	4355								
Db	2392	ETANEENTFMKNVLKTNFK	----	MNQLTOELFSLKRRER-ESVEKIQSPENS	----	VNVAI	2444				
Qy	4356	EGGDKLEAFNFCBDAIFEMTHASGLMAASEBSVGGTKNREASVYMWGDDDDDERAGKO	4415								
Db	2445	DHLSKOPLEVLVTEBALKSLENQOTYFKSFEENGKSGIINLETRLLQL	----	ESTVSAKO	2501						
Qy	4416	PFRRLGQSKVDGATVATFSSLSPSNIIKAKTIADMQOMPFAELAVGFFKXFFVFIYYLGVG	4474								





QY	1891	IAESITEISNLYSPFFLEVA-----REF-----VMOQALAEAVE	1924
Db	161	LACKQHEIEELARELEEMRVYGTBGLQLOQFEFAAIKQRDGIITQLTANLQARREKDE	220
QY	1925	T-----NQVNRDPVGGNGENLFLPLIKVLDRLLLVGMRRDEDEVKL	1966
Db	221	TWREFLELTQSQKLOIQOQLQASSETLRNTHSTASTADLLQAKQOILTHQOQLEODHL	280
QY	1967	L-----IWNPNETWDPSPFDKGGDKHRKGL-----LHMMAEGCAK	2001
Db	281	LEDYQKKKEDFTWQISFQOEKIKYEMQODKVENSNKEBIOKETIIEBELNTHKIEEEK	340
QY	2002	LQMCYLLOHLNDIQLRHRVEAIIAPAFHFDVGLQDQLRRYTEIKQSDPLPSAVAAKKTR	2061
Db	341	-----KTLELKDK-----LTTADKLGBELQBOIVQKQOEIKNMKLELTSKQKERQ	386
QY	2062	FRCPPEQNAILSF-----KHLBEDKENCPCGEBELIARNWEPHDTLMA	2106
Db	387	SSEETIKQLMGTVEELQKRNHKDSQPETDIVORMEQETQKLL-----EOLRAELDEMUGQOIV	443
QY	2107	HVSLHALQEPDAENQOEPAKPGAGKLYNII-----	2138
Db	444	QMKQELIROHMA---QMEEMKTRHKGEMENALRSYSNITVNEDQIKLMNVAINELNKLQ	500
QY	2139	--NTVKE-LEEBAKAIEBPPTPEEKFRKVLIOFI-----VNWABESQIETPKLVREM	2189
Db	501	DTNSQKEKLEELGILILE--EKALQORQLEDLVELSFSRBOIQARQTTABQESKLENEA	558
QY	2190	FSLLVROYDAVGELIRALE-----KTVYVINAKTKLDVAEMVMWGLSQIRALLPVQMS	2240
Db	559	HKSLSVTEDLKAIEIVSASBSRKEBELKHEAEVTNYKIKLEMLE-----KEKNVLDRAAE	613
QY	2241	QEBEELMRKWLKLVNNHTFFOHPDLIRVLR-----VHENVMVMNTLGRRAQAOQSDA-	2294
Db	614	SOEAELERLR-----TQLLSHSEBELSKLEBDELBIEHRINIEKLNGLGHIHYKQOJDGL	667
QY	2295	-QPSSQPAEADSKEKDTSHEMVVACRCFLCYFCRTGRQNKQAMPDHFDFLLIENSNILSR	2353
Db	668	QNEMSKQIETMQPEKDN-----LITKQNO-----LILIEISKLDLQ	703
QY	2354	PSL--RGSTPLDVAYSSLMNTALALAREHYLEKIAYVLSRCGLQNSSELVEKGYDPLG	2411
Db	704	QSLVNSKSEMTLQINELQKEIEI---LRQEBKEKGTLEQEVQVELQLKTLELLERQMKKE	760
QY	2412	WD-----PVGERYLDFLRCVWNGESVEENANL	2441
Db	761	NDLQEKFAQLEAENSILKDEKTKLTEDMLKIHTPVSQEBRLIFLDSIKSKSDSVWEKE--	818
QY	2442	VIRLLIRREPECLGALRGEGELLKAIVDANKMSERIAADRKLREMEQEGDVNPSHPLPE	2501
Db	819	-HEILLE-----ENEDLKQOCTLNEEIEK--QRWTFSEAKNPFVNY-----	858
QY	2502	SDEDEDYIDTGAAILNFYCTLVDLLGRCPADAGVIALGKN--ESLRARAILRSLVPLEDLQ	2560
Db	859	QELQEEY-----ACLLKVKODLED-----SKNKQELEYSKKLKALNEELHLQ	900
QY	2561	GVLSLRFTLNPAAGEERPKSDMPGSLIPGHKQSVGLFLE--RVYGIETQELFKVLEEA	2618
Db	901	RI-----NPTTVK-----MKSVFDEKDTFVAETLEMGVEVVEKDTTELMEK--LEV	945
QY	2619	FLPDLRAATMLDRNDCESDMALSMNR-----YIGNSI-----LPLLI	2656
Db	946	KREKLELSQRL-----SDLSEQLKQKHGEISFLNEEVSLSLQKEQVSLRCELELII	998
QY	2657	KHAYFYNEAEN-----YASLLDATL-----HTVYRLSKN-----R	2686
Db	999	NH-----NRAENVQSCDTQVSSLLDGWVTWTSRGAEGSVSKVNSKSGEESKIMVEDKVSFE	1054
QY	2687	MLTKG-----QREAVSDFLVALTS-----ANQPSMLLKLRKLTVDVSKLSEYTTVALRLL	2737
Db	1055	NMTVGBESKQEQILHDLPLSVTKESSLRATOPSENDKLQKELNVLKSPQND-----LRLQ	1109



Db 1910 L A V E L S K A E G V I D G - - - - - Y A D E K T L F E R - - - - - Q I O K T D I I D R L E 1946  
Qy 3765 Q T S L H S I P R H R A C N I F A R T Y Y E L M L E E N I Q I E V M I - - - - - E D L T Q S F E 3808  
Db 1947 Q E L L C A S N R - - - - - L Q E L A E Q Q I Q E R E L L S R O K E A M K A E A G P V E Q L L Q E T E 1996  
Qy 3809 D A E L U K S D V B E G E K P D L T O L V T T F R G A M T E R S G A L Q E D P L Y M S Y A H I A K S C G E E E 3868  
Db 1997 K L M K E L V O C A E K - - - - - V R D D L O K V K A L E I D - - - - - 2026  
Qy 3869 E G G E E E G G E A E A D E G R A S I - - - - - H E Q E M E K Q - - - - - K L I F H O A - - - - - R L A D R G V A E M 3916  
Db 2027 - - - - - V E E Q S R F I E L E Q E K N T E L M D L R Q O N Q A L E K Q K R K F D E Q A I D R E H R D V F Q Q 2082  
Qy 3917 V L L H I S A S K G L P S E M V M K T L G I S I L R G G N I D I Q M G M L N H L K D K D V G F T S T A G L M N S 3976  
Db 2083 E I Q K L - - - - - E Q L K V V R F Q P I S E H Q T R E V E Q - L A N H L K E K T D - - - - - K C S E L L S 2128  
Qy 3977 C S V I D L D A F E R N T K A E G L V G L E G A G E K N H D A E - - - - - F T C A L F R F I Q L T C E G H N I D W Q 4032  
Db 2129 K E Q L Q R D I Q E R N E I E K L - - - - - E F R V R E L E Q A L L V S A D T F Q K V E - - - - - D R K 2171  
Qy 4033 N Y L R T Q A G N T T V N V I C T D Y L L R L Q E S I M D F Y M H Y S S K E L I D P A K A N F F K A I G V A S Q 4092  
Db 2172 H F G A V E A K P E L S L E V - - - - - Q I O A E R D A I D - - - - - R K E K I T N L E S Q L E O F R - - - - - E E 2215  
Qy 4093 V F N T L T E I Q I P C T Q N Q O A L A H S R L W D A V G F L F L G H M Q D K L G K H S Q V - - - - - D L L K E L L 4149  
Db 2216 L E N K N E E V Q Q - - - - - L H M Q L E I Q K E S T T R L Q E L E Q E N K 2249  
Qy 4150 N L Q K D M I P M M L S M L E G N V N G T I Q K M V D T L V E S A S N V E L I L K Y F D M P L K L D I T S S A S F 4209  
Db 2250 L F K D M E K L G L A I K E S D A M - - - - - S T Q O H V L F G K F A Q I I O E K V - - - - - 2289  
Qy 4210 Q E I D A N D G W L P K D F K E M E Q K S Y T P E - - - - - E I E F L L A - - - - - C C E T N 4250  
Db 2290 - E I D O L N E Q - - - - - V T K Q Q O L K I T D N K V I E K N E L I R D L E T Q I E C L M S D Q C V K R N 2341  
Qy 4251 H D G K L D Y I G - F C D R F H P A K E I G F N L A V L T N L S E H - - - - - M P N E P R L A R F L E T 4298  
Db 2342 R E E I E Q L N E V I E K L Q E L A N I G Q T S N N A H S L S E A D S L K H Q L D V V I A E K L A L E Q Q V E T 2401  
Qy 4299 A G S V L N F E P P L G R I E M G S K R I E R V Y F E I K E S N I E O W E K P Q - I K S K R A F F Y S I V T E G 4357  
Db 2402 A N E E M T F M K N V L K E T N F K - - - - - M N Q L T Q E L F S L K R E R - E S V E K I Q S I P E N S - - - - - V N V A I D H 2454  
Qy 4358 G D K E K L E A F N F C D A I F E M T H A S G L M A A S E S V G G T K N R E A S Y M Y M G D D D D E R A G K D - P 4416  
Db 2455 L S K D K P E L V V L T E D A L K S L E N Q T Y F K S F E N G K G S I I N L R L Q L - - - - - E S T V S A K D L E 2511  
Qy 4417 F R R G L Q S V K G V A T A F S L S P S N I K A K I A D M Q M P P A E L A V G F F K M F Y L F Y I L G Y G V L V 4476  
Db 2512 L T Q C Y K I Q D - - - - - M Q E O G F E T E M L Q K I V N I Q I V E E K V A A L Y S Q I - - - - - Q L E A 2560  
Qy 4477 V V R Y I F G V L L G M R G P Q D E P P P P E T B E E K T G O L R H R L L A T Q S R H P A L P A D P A D T G O M Q 4536  
Db 2561 V Q E Y - - - - - A K F C D N Q T I S E P E R T N I Q N L R E - - - - - D E L G S - D 2597  
Qy 4537 V S A F G L D I T K E D N G Q I Q V K P H E S P S T S P S G E A E V S P D S A D H T E Q R P P S I D I L G G 4596  
Db 2598 I S A U T L R I S E L S Q V E M - - - - - H T S L I L E K Q V E I A E K N V L E - - - - - K E K L L E L O K L E G 2649  
Qy 4597 E O A K Q A Q E R M E A Q A A Q A M A S A I E A E S K A V Q G - - - - - P A P S A L S Q V D L S Q Y T R R A 4648  
Db 2650 N E K K Q R E K E K R S Q D V E V L K T T T E L F H S N E S G F F N E L R A L R A E S V A T K A E L A S Y K E K A 2709

RESULT 7

US-11-090-997-868

; Sequence 868, Application US/11090997

; Publication No. US2006021672A1

; GENERAL INFORMATION:

; APPLICANT: Betsholtz, Christer et. al.  
; TITLE OF INVENTION: Glomerular Expression Profiling  
; FILE REFERENCE: 04-1059  
; CURRENT APPLICATION NUMBER: US/11/090,997  
; CURRENT FILING DATE: 2005-03-25  
; NUMBER OF SEQ ID NOS: 2985  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 868  
; LENGTH: 3907  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-090-997-868

Query Match 1.1%; Score 301.5; DB 7; Length 3907;  
Best Local Similarity 17.9%; Pred. No. 1e-08;  
Matches 592; Conservative 458; Mismatches 1161; Indels 1089; Gaps 140;  
Qy 1800 A A H A L C T H V D K O L - - L Y A I Q S O Y M - - - - - S G P L - - - - - R Q G F Y D L L I A L H L 1839  
Db 51 A H D L - - N I D O S O C N E M Y I N S S O R V E S T V I P E S T I M R T L H S G E I T S H E Q F - - - - - S V E L 103  
Qy 1840 E S H - A T T M E A C K N E - - - - - F V I P L G P E L K A L Y E E P - - - - - D M G H S L R S L Q T S V R P Q M K W T D 1890  
Db 104 E S S I T T A D C S E V N G C S F V M R T K P T N L L R E E F G V D D S Y S E Q G A Q D S P T H L E M M E S E 163  
Qy 1891 I A E S I T S N L Y S P Y P L E V A - - - - - R E F - - - - - V M Q A L A E A V E 1924  
Db 164 L A G K Q H E I E L N R E L E E M R V Y T G E L Q L Q E F A A I K O R D G I I T O I T A N L Q Q A R R E K D E 223  
Qy 1925 T - - - - - N O V H N R D P V G G S N E N L F L P L I K L V D R L L L V G M R D E D E V K L 1966  
Db 224 T M R E F L E T S Q S K L Q I O F Q O L Q A S E T L R N S T H S S T A A D L L Q A K Q I L T H Q Q L E E Q D H L 283  
Qy 1967 L - - - - - I M T N P E T W P S F D K E G K D E H R K G L - - - - - L H M Q A E G A K 2001  
Db 284 L E D Y Q K K E D F T M Q I S F L Q S K I K V Y E M E Q D K K V E N S K E E I Q E K E T I I E L N T K I I E E K 343  
Qy 2002 L Q M C Y L L O H L N D I Q L R H R V E A I T A F A H D F V G D I Q T D Q L R Y T E I K O S D L S A V A A K T R E 2061  
Db 344 - - - - - K T L E K D K - - - - - L T T A D K L G L E Q I V Q K N Q E I K N K M L E T N S K Q E R Q 389  
Qy 2062 F R C P P R E Q M A I L S F - - - - - K H L E E D K E N C P C E E L I A R M N E P H D T L M A 2106  
Db 390 S S E I Q L M G T V E L Q R N H K D S Q F E T D I V Q R M E O E T Q R K L - - - - - E Q L R A E L D E M Y G Q I V 446  
Qy 2107 H V S L H A L Q E P A A E N O P E A K P G A F G K L Y N I I - - - - - 2138  
Db 447 Q M K Q E L I R Q H M A - - - - - Q M E E M K T R H K G E M E N A L R S Y N I T V N E D Q I K L M V A I N E L N I K L Q 503  
Qy 2139 - - - - - N T V K E - L E E E A K A I E E P K T P E E K F R K V L I Q T I - - - - - V N M A E S Q I E T P K L V R E M 2189  
Db 504 D T N S Q K E K L E E L G L I L E - - - - - E K C A L Q R Q E D L V E E L S F S R E Q I Q R A Q T I A E Q S K U N E A 561  
Qy 2190 F S L L V R Q Y D A V G L I R A L E - - - - - K T Y V I N A K T L D V A E M M V G L S Q I R A L L P V Q M S 2240  
Db 562 H K S L S T V E D L K A I V S A S E S R K S L E L K H E A E V N Y K I L E M L E - - - - - K E K N A V L D R M A E 616  
Qy 2241 Q B E E E L M R K L W L V N N H T F F Q H P D L I R V L R - - - - - V H E N V M A V M M T L G R R A Q A Q S D A - 2294  
Db 617 S Q A E L E R L A - - - - - T Q L L F S H E E E L S K L E D L E I E H R I N I E K L D N L G I H Y K Q Q I D G L 670  
Qy 2295 - Q S S Q P V A E D S E K E T S H E M V V A C C R F L C Y F C T G R Q N Q K A M P D H F D F L L E N S I L L S R 2353  
Db 671 Q N E M S Q I E T M Q P E K D N - - - - - L I T K Q N Q - - - - - L I L E I S K L D L Q 706  
Qy 2354 P S L - - R G S T P L D V A Y S S L M E N T E L A L R E H Y L E K I A V L S R C G L S Q S N E L S E V E K Y P D L G 2411  
Db 707 Q S L V N S K S E E M T L Q I N E L Q E I E I - - - - - J R E E K E K G T L E Q E V Q E L Q L K T E L L E K Q M K E K E 763  
Qy 2412 W D - - - - - P V E G E R Y L D F L R F C V W N G S E E V E E N A N L 2441  
Db 764 N D L Q E K F A Q L E A E N S I L K D E K T L E D M L K I T H T P V S Q E R L I F L D S I K S K S D S V E K E - - - 821



Db 2458 LSKDKPEVLVLTEDALKSLNQTIFYKSPBENGKSGSIINLETLLQL---ESTVSAKDL 2514  
 Qy 4417 FRRLGQSKDGVATAFSSLSPSNIKAKIADMQQMPAELAVGFPMFFYLFYVLGYGLV 4476  
 Db 2515 LTQCYKQIKD--MQEQQFETEMLQKKIVNLQKIVBEKVAALVSQI-----QLEA 2563  
 Qy 4477 VVRYIFGVLGLMRGPOTDEPPPTPEEEXIGQLRHRLLATQSSRHLPALPPADTQMQ 4536  
 Db 2564 VQEY-----AKFCQDQTISSPERTIQLNQLRE-----DELGS-D 2600  
 Qy 4537 VSAGFLDITKEDNGIQVKPHESPSTSTPSSGGEAEVSPDESADHTEEQRPPLIDLGG 4596  
 Db 2601 ISALTALRISELESQVEM-----HTSLILEKEQVEIAEKNVLE--KEKKLLEQLKLEG 2652  
 Qy 4597 EQAKKQAEQERMEAAQAQAAMSAIEASKKAVQ-----PAPSALSQVDLSQYTRRA 4648  
 Db 2653 NEKKOREKEKRSQPDVEVLKTTTTFHPSNEESGFNELEALRAESVATKAELASYKEA 2712  
  
 RESULT 8  
 US-10-505-928-325  
 ; Sequence 325, Application US/10505928  
 ; Publication No. US20060088532a1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505,928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO 325  
 ; LENGTH: 3113  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-505-928-325

Db	361	----	EOKLK-----	KLTEDLSQORNAESARCSLEQKI	KEKEKEFEQEBLSRQORSFQTL	410	
Qy	2168	----	IQTIVNVAEESQIETPKLVREMFSLVRQYDAVBELIRALEKTYVINAKTKLDVAE	2223			
Db	411	QDQCIQW	KARLTQELQ-----	QAKNMHNVLAQELDKLTSVKQLENN-LEEFKQKLCRAE	464		
Qy	2224	MWVGLSG	QIRALLPVQMSQBEELMRK-RLWKL	VNNHTFFQHPDLIRVLAVHENVMAVMN	2282		
Db	465	QAFQASQIK-----	ENELRRSMEEMKKN-----	LLKSHSEQKAREVC	503		
Qy	2283	TLGRRAQASDAQSPQVAEDSKEKDT	HEMVVACCRFLCYFCRTGRNQKAMDFHDF	2342			
Db	504	HLEAELKNTIKQCINQSONFAEEMKAKNT	SOETWL-----	RDQEKINOQ-----	547		
Qy	2343	LLSNSILLSRPSLGRSTPLDVAYSIML	TELA---LALREHYLEKIAVYLSRCGLQSN	2399			
Db	548	--ENSLTL-----	EKLKLA	VDLEKORDCSQDLLKKREHHIEQLDKLSKTEKESK	596		
Qy	2400	S-----	ELVEKGYDPLGWDVPBGERVLDPLRPCW-----	VNGESVEENA-----	2439		
Db	597	ALLSALELKKEY-----	ELKEEKL-----	FSCWSENEKLLTQWSEKENIQSKINH	646		
Qy	2440	-----	NLVIRLLIRRPCLGRPELALRGE	GEGLLKATVDANKMSERIADRRKL	2485		
Db	647	ETCLTKTOQIKSHYNERVTRLEMDRENLS	VEIRN-----	LHNVDLSKSV-----	VETQKLA	698	
Qy	2486	EMOEGDVNFS-----	HPL-----	PESEDEDEYIDTGA	2514		
Db	699	YMELOQKA	EFSDQKHQEIENMCLKT	SQLTQGVEDLEHKLQLLSNEIMDKORCYQDLHAE	758		
Qy	2515	ILNFYCTV	DLGLRCAPDAGVIA-----	-----	2537		
Db	759	-----	YESLRDLLK--SKDASLVTNED	QHSLLAFDQQPAMHHSFANIIGEQSMP	SERSE	812	
Qy	2538	--LQKNE	SLRRAILSLVPLEDLQVLSL	RFTLNNPAAGEERP	PKSDMPSGLIPGHQKQSV	2595	
Db	813	CRLEADQSPK	SAILNRVD-----	SLEFSLES-----	QKMNSDL-----	QKQCE	853
Qy	2596	GLF-----	LERVYGIETQELFYKLL	EEAFPLDLRAATMLDR-----	-----	2631	
Db	854	ELVQIKGEI	ENLMKAEQHQSFVETSQ	RIKSLQEDTSAHQNVVAETLSALENKEKELQ	913		
Qy	2632	--NDGCE	SDMALSNRYIGNSILPLIKHAYFY	NEAENVASLLDATLHTVYRLSKRMILT	2689		
Db	914	LLNDKVETE	QAEIQELKSKNHLLED	SLKQLLSET---LSLEKEMSSII	SLNKREIEE	970	
Qy	2690	KQREAVSDF	VALTSMQPSMLLK-----	LLRKLTVDPVSKLS-EYTTVALRLLTLHYE	2742		
Db	971	LTQENGTLKE	INASLQEKNNLQKSESFANY	IDEREKISLSESDQYKQEKLLTLL-----	Q	1026	
Qy	2743	RCAKYGYSTGAGQ	AGFASDDEKRLTMFLFSNIFDSL-----	SKMDYBPFLFGKA-LPC	2796		
Db	1027	RCBETGNAY	EDLQKYKAAQEKNSKLECLL--	NECTSLCENRKNLEQLKEAKEHQEF	1084		
Qy	2797	LIAIGCALPP	DISL-----	SKNYDDFEYKQQAAGDLPNDPQDPINTSSVA	2844		
Db	1085	LTKLAF	AEARNQNLMLETVQALRSEM	TDNQNSKSEAGG---LKQIMTLKBEQNK	1140		
Qy	2845	LNNDLNTIVQK-----	-----	FSEHYHDWASRKIENGWYVYEGWSDSQKTHP	2887		
Db	1141	MQKEVNDLLO	QENQMLKMWKTKHECQNLSESEP	IRNSVYKRESERNQCNFKPQMDLVEK	1200		
Qy	2888	RLKPEYN-----	MLND-----	YEKERYKEPVRESIKALLAIGWSVEHSEVDIPSNRS	2934		
Db	1201	SLDSYN	QALVQLEAMLNKLKLQES	EKECICLOHELOTIRG-----	DLETSNLQ	1250	
Qy	2935	SMRRQSKSGR	PPETVTDSTPDPNPHVDMNTLS	REMQNMAERLADNAHDIWAKKK	2994		
Db	1251	DMQSQEIS	GLKDCET--DAEEKYIS	GPHELSTS-----	QN-----	DNAH-----	1287
Qy	2995	KEELVTTGGG	IHPOLVPYDILLTTOKEKKORERQ	EFKLYOQYKHLRFSKAPQSDTEQ	3054		
Db	1288	-----	LOCSLQTTMKNLNELEKI	CEI-----	LOAEKYLVELTNDORSCEIT	1329	



```
; SEQ ID NO 10
; LENGTH: 3811
; TYPE: PRF
; ORGANISM: Mus musculus
US-11-090-997-10

Query Match      0.9%; Score 253.5; DB 7; Length 3811;
Best Local Similarity 17.0%; Pred. No. 9.6e-06;
Matches 660; Conservative 560; Mismatches 1411; Indels 1245; Gaps 157;

Qy 1249 QPIFENTDEMTDRIDVT-----RIPAGSDTPPCLKISHNTTETMEKANWELRLSLP 1301
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 542 QTIAEQENRLESEARKSLSTVEDLKAEIVAASESKELELKHAEITNYKIKLEMLEKE-- 599
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1302 VICNEFID-----EAKARWVEIKORQI-LMKEAVEAQMPAHIQIMRSGFTMN 1352
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 600 --KNAVLDRAESQEAELERLTQLLFSHBEELSKELEDLEVEHRIENK-----LK 649
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1353 DIKGLHYEDNQELPSSKNKELPSRPPRKSGMTGRVTION-----YNNLQPGQVNG- 1403
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 650 DNLGIHYKQIQDGLQENMRKQESMQCETDNL-----ITQOQLIILENSKJRDLOECLVNSK 706
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1404 -----MHRSTSAEMAKYDLGAQGLTPDDKDKGRSPKFPFRSKRGESSDRAKSRKS 1456
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 707 SEEMNLQINELQKEIEILKQEKKEKGLQEQVE-----LQLKTEQLEKQLEKED 757
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1457 KTPDPFS--DTEVSPERGARRP-NPQIKV-SQANQRYNGMNPARTNLVGSQVGLNNA- 1511
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 758 DLQEKCAQLDAENILKEEKVLEDKLMYSPSQEERSIADVPSTKSADSRMQKEVAM 817
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1512 --TPTQBRKQ--MTTSTLAQSAETVGNIEIPAECCLKLINEFYGVRIYPGQDPHYV 1565
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 818 LRKETDLQOQCLYLNBEIEKORNTFAPEAKNFVNYQELQREYTCLLKI----- 867
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1566 IGWTTQVHLHSKDFNOSKVTKSSVIITDDYD---RVVENVRQSCYVMRADELYNEWMA 1622
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 868 -----RDLEATQTKQAL-----EYESKLRALE-----EELLSKRG 899
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1623 EATAKAGSQGMF-----IGCSVDTSVSGVSFTCEGKDTSPFKWPEPETKLPFAIFVEAT 1676
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 900 PAAPKGKSSGIFPSETLEIGEVVEKDTTEL---MEKLEVTREKLELSEK-----VSG 950
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1677 SKEILOELGRSATSPLSAAVLFTSDKHVTPPPRLKQVCLKPHQWAR----- 1726
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 951 SEQLKQTH-----CTINSLSAEV-----RALKQBEQLLRCGSELELLANPGSTENA 1000
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1727 -VPNQLQVHAL--KLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHS 1783
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1001 PVQSSSYQAGLVMGKVGDSGG-----SISKISKDLAESK-----PMIEDKIPKES 1047
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1784 HTLLTYAALCYQSNYRAAHALCTHVDQKQLLYATQSQYMSGFLRQGFYDILLIALHLSHA 1843
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1048 GREQLLLPTRAQKPSHATVPECESEKQQLQELHALKAEQDLDLRLQWEAQRICLFFVYVSTHA 1107
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1844 TTMEACKNEFVPLGPPELKALIEYEDMGHSLSRLQTESVRPQMKMTDIASITISNLYS 1903
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1108 DQVRA-----HMEKREBEALCSLDELISAQKKID-----ELHKQHQ 1145
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1904 PYF-----PLEVAREFVMQALAEAVETNQVHNRDPVGGSGNENLFLPLIKLVDR 1952
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1146 COLQNFKIQTGDEPLQVLIERLOQAVSEK-----FHISKTLNNVFECYTP----- 1193
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1953 LLVGMNRDEDVEKLLIMT-----NPETWDPSPDKGDKDEHRRKGLLHMKAEGAKLQMCYLL 2008
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1194 -LKCEMNEEKENSGVYTSQNSQSPQLQRYEVQDFQESQMVLGKVTCECKLS--GLQ 1250
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2009 QHLNDIQLRHVRVIAIIAPAHDFVGLQTDQLR-----RYTEIK-QSDLPSPA 2060
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1251 TRLGKIHEQQTDGVALFEPAEQAAEAEAGLLSGCSQSALQSTDVLSKVSLSPEAKSR 1310
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 2061 EFRCPPEOMNAILSFK-HLEEDKENCPCGEELIARMEPHDTLMAHVSJLHALQEPDAA 2119
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1311 ECERQVQLQSPVAAGQLQLTETETANHRAETESLQORLEAVE-----APVQPSLS 1361
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

2120 ENQPEAKPGAFGKLY-----NIINTVK-----ELEBEAKAI-----EPPKKTPEKFR 2164
1362 IDSVFPGSGAQRVPVYCGSCLRECVGTAKFSDFEVRQETNNMWNLMMEKQYQERLEBEIA 1421
2165 KVLIOITVNAWESQIE-----YD-----AVGELIRALEKTYVINAKT 2217
1422 KVIIVMSIAFAQQTELSRLSEGKENTIQSEQAHTLCSQNKHQLNDITSQSOVQLQTFEAT 1481
1482 DKNFKEEFPLSKELGEYRKAVPLSSHDDDDILKSEEHGLAISEEIFSKDETPIVRKSM 1541
2218 KLDVAEMWVGLSQIRALLPVQMSQEBEELMRKLMKLVNNHTFFQHPDLIRLVLRVHENV 2277
1542 HDEVLVSSMDTISR-QUILNEQLEDMRQELVRQ-----YEEHQOQATEMLR----- 1584
2278 AVMMNTLGRRAQASDAQSSQPAVEDSKEK---DTSH-----EMVVA 2317
1585 QAHHQMERQERQEQLOEBEIKRLNEQLAQSSIDTEHVVSERERVLLLEEALKQLPLA 1644
2318 CCRFLCYFCRTGRQNKAMPDHFDFLENSNILLSRPSLRGSLDPLDVAYSLSMENTELAL 2377
1645 GRKELC--CELRRSSTQTQGHDDQVEEOTL---KOKTLERSPEDALLDRNLSNERYAL 1699
2378 ALREHYLEKIAVYLSR-----CGL-----QSNSELVEKGYPDLG---WDP 2414
1700 KKANNRLKILLEVVKTTSAAETIGHVLGILDRSKGQTASSLLMRSSADASATTCAP 1759
2415 VEGERYLD-----FLRFCVWNGESVEENANLVRILLIRPECLGPALRGEGEG 2463
1760 EDCARAMDESIPSPYGTATATHDSIW--SKVTEGAELSQRLV--RSGFAGPVIDPENEE 1815
2464 LLKAIVDANKMSERIADRRKLRMEWQEGDVNFSHPLPESDE--DEDVIDTGAAILNFYCT 2521
1816 LM-----LNISSRLQAAVEKLEAISETNTQLEHAKVTQTELMRESPROQEAETESLHC- 1869
2522 LVDLGRCAPDAGVIALGKNESIRARAILRSVLPLEDQGLVLSLRFLLNPPAAGEERPKS 2581
1870 LEELRERL-----QESRAREQL-----AEELNKA 1894
2582 DMPGSLIPGHKQSVGLFLERVYGIETQELFYKLLLEAFLPDLRAATMLDNDGCESDMAL 2641
1895 E---SWIDGVSDKTLFERQIQ--EKTDIIEHLEQEVL-----CANNRLQELLESOR- 1941
2642 SMNRYIGNSLPLLIKHAVPYNEAENYASLLDATHVTYVLSKNRMLTKQOREAV----- 2696
1942 -----RVEERQLLCQREAMRAEAG 1962
2697 ---SDFLVALTSAMQPSM-----LLKLLRKLTVDSVKLSYTTVALRLLTLHY 2741
1963 FVEQQFLQETEKLMKEKLELVQCAEKVRGLOQKVKALEIDVEE-----QVSRFIELEQ 2016
2742 ERCAKYVSGTGAQGAAGFAGASSDEEKRLTMMFLSNIFDSLKMDYPEPELFGKALPCIIAIG 2801
2017 EKNAELTDLRQQSQAL-----EKQLEKM----- 2039
2802 CALPPDYSLSKYDDDEFYKGEQAAGDLNPDQDPQINTSSVALNNDLNTIVOKFSHYH 2861
2040 -----RKFLDE-----QAID-----REHER 2054
2862 DAWAS--KRIENGWVYGEHSDSQKTHPRLPKPNMLNDYKERYKEPVRESLKALLAIGW 2919
2055 DVFQEQIQKLEH-----QLKAVPRIQPVSEHQAREVEQTLNHLKTKTORCSLELL 2104
2920 SVSHSEVDIPSNKRSMRROSQSGRPPEIVTDSATPF-----DYNPHFVDMTNLTLSREM 2975
2105 SKQLQBDIQERNEETEKLECRVRELEQALLA-SAEFPFKVEDQKRGSAVEADPELSLEV 2163
2976 QNMAERLADNAHIWAKKKKEELVTNGGGHLPOLPYVDLLTIDKKEKKORSQEFBLKYLV 3035
2164 QLQVER-----DATDRKQKE--ITN---LEEQLQEP---REELKNKNDEQVLLMQLE 2208
```

Qy	3036	YQGYKLRHPSKAPQSDTEQTTTGVATIELRFAYSLLEKLIQYIDRATINMKLLXPSTTFSR	3099
Db	2209	IQ-----RKESTTTLQELQQ-----ENRUFKDEIEKL-----GFAM	2239
Qy	3096	RSSEFKTSTRD- IKFFSKAVLPLMEKYFSTHR--NYFIAV-----ATATNVGAASLKEKE	3147
Db	2240	KESDSVSTRQOPMLFGKPAQLIOEKEIIEIDRIAEQFIKQQQLKLTIDNKV---IEEQKE	2296
Qy	3148	MVAALFCKLASLRSR-----LAAFGPDVRITVRCLQVLVKG-----	3184
Db	2297	QIQDLEQIETRIELMSEREHEKKQREVEEQLTGVVEKIQBQVWSTEQOREGARTLPEDEES	2356
Qy	3185	-----IDAKSLVONCEPIFIRTSMLTFFNNV-----ADDVGHITMNLQDKYAHLRG	3230
Db	2357	FXHQLDVTAEKLVLEQOQVETTTQQWTHMMNVLKEINFKMDQITQSLCNLN-----	2407
Qy	3231	THLKTSTSLGVINGVLLIPILITAKFDHLANCEYGADILLDEIQVASYKMLGSLVALGTDAS	3290
Db	2408	-----KECAS-----NEELPSLPKESVHMTVHELGSNDLQPDAPAQ-----DVTPLPEKQTS	2455
Qy	3291	LTHDRKYLKTEIERHKPALGSCLCGAFSSTFPVAFLEPHLNKHNQFSLNRIADHSLAEQD	3350
Db	2456	LTRLQKSPASARTQIEISLASSVG-----HVNMTVAE-----HMNOLLKNVLK	2482
Qy	3351	IMQMEQOMPTLETILGEVQDFVESDKTYNE-----APHIIDVVLPLLCSYLP	3398
Db	2483	V--ELTQCREQTETIQBQAQS--ETDRLOKKLTDLQRLSEKFAALVSQVQMEAAQBYVP	2538
Qy	3399	FWAQAGPDNVP-----TGGN-----HVTMTVAE-----HMNOLLKNVLK	3433
Db	2539	FHOEKQVSSAPGSDTQONANGLTGASTESLIPVTUURLAEVSRAEVHSGTMSEKLVG	2598
Qy	3434	LIKQIGNENAPWMTRIATYQTQIIINSSEEL-----LRDSFL-----	3471
Db	2599	IVGNASE-----TEKRVIELQKLEEAERPEEGEQSSRDGEVRESYMTSLQKDLQG	2652
Qy	3472	---PLAE-----RVKRKTDMMFKBESLR-----GFTKSSTDDTSQVESQIQED	3512
Db	2653	VKDPLTEAKEKLSYLEKEKRTQGESREAPIPEPPSVVEVGGCSGLTERTDKVSSSGNOT	2712
Qy	3513	WOLLVRDIYSFYPLLIKYVDLORN-----HMLRNNVPEAEELYNHVAREFINWS-	3561
Db	2713	LQIILLRD-----AAIQTDLQSESSQBEVRDITNQLTKKXHEIQEL--HAAEILDMESR	2763
Qy	3562	-----KSOYF-----LKEBQNFISANE-----IDNNVLLIMPTATRRVTAVTD	3598
Db	2764	HILETESLKXEHYVAIQLLTKECTELKEMTQCLCKEGSSIPELADSVAVQSREVYS-SD	2822
Qy	3599	GTPGGGKKKKHRDKRDKQVOASLWACLRLLPV-----GLNLPAGREOELVQHKC	3654
Db	2823	SESDWQSQGFDTAIEGRE-EGETSADLPFKPIKGLVKAHVSEGMQVLS-LSSPLCDGGE	2880
Qy	3655	DRFLKXSEQDVAE---FAKTQLTLPDKIDPADEMSQHVLYSLKSGSKSNITVEI-AE	3710
Db	2881	DRSIQOLSESILKGRQAYLNTISLKLII-----SKMQVRRETEVY	2921
Qy	3711	NKAXIIDDTVERIVAMSKVLFGLMIDHPQOMSKNNYRSVVSIQRKRAVIACFQTSLSHS	3770
Db	2922	DRCHLSWRGELLACQRFI-----KERSVLLATFQETLTS	2958
Qy	3771	LPRHRACNIFARTYYEULWLEENIGOEMYIEDLTQSFEDAELKXSDVVVEGEEKPDPPTQL	3830
Db	2959	LSTRDV-----DGLNLSLQRIQEOGIEVHTAMDCLQAD-----	2993
Qy	3831	VTTFCRGANTRBSGALQBDPLYMSVAHIIAKSCSEEBEGGE---BEEGGGEAAEADeg	3887
Db	2994	-----RRS-----LLAEIEDLRAQINGKGVKTLREOQTEKSSQELL	3029
Qy	3888	RASIH-----BOEMEKOKLLFHQARLADRGAEMVLLHIISASKGLPSPEVMWMTLQLGTSI	3942
Db	3030	DCSMQOKOSLEWQJLSELSLRDAELQBLQSEKXVV-----AELKSELAQAKLELGTTL	3084
Qy	3943	-LRGNIDIQGMNLNHLKDKDKDVGFFTS IAGLMNCSCLVDLID-APFRNTKAEGLGVGLG	4000

Db	3085	KAGHKLELEAPRSEVKETDEIHPLSDTLAREQKNSLELQWALEKARSQHSGRE-	3143
Qy	4001	AAGEKNHDAEFTCALFRFIQLTCGHNLDWQNYLRTQAGNTTTVNVVICTDYLLRLQE	4060
Db	3144	---KBELEDLKFS---LEDQKRRNTQLNL---LLEQOK	3172
Qy	4061	SIMDFYWHYSSKELIDPAGKANFFKAIGVASQVFNLTLEVIQGPCTQOQALAHSLMDA	4120
Db	3173	QLLN-----ESQKI-----ESQMLHDAQLSEE	3196
Qy	4121	VGGFLFESHMQDKLSKHSSQVDLLKELLNLQDMIPMLSMLEGN-----VVGFTIGXQ	4175
Db	3197	QGRNIGL-----QALLSEQVRIQESKSTLDKERELVAQLQSRDGGOPPAPLPSEDLLKE	3252
Qy	4176	MVDTLVESASNVELIILKYFDMFLKLDLTSASFQIDANNQGWLPKOFKEKWEOKSY	4235
Db	3253	LQQLBEKHSRIVELLSETEKY-KLDSLOTQOME-----KDRQVHQKTL	3296
Qy	4236	TPSEIEFLLACCTNHGDKLDYIGFCORPHEPAKEIGFNLAULLTNLSEHMPNEPLARF	4295
Db	3297	OTTO-----BANTQO-----KMQEQLQSKVEELQRLQLEKROQ-----	3330
Qy	4296	LETAGSVLNYFPFLGRIEIMGSGKRIERYFIKESNIEQWPKPOIKSGKRAFFYSIVT	4355
Db	3331	-----VYKLDLEG---KRLQGLMQSQFOELEPEEK-----	3359
Qy	4356	EGGDKLEAFVNFCEDAIFEMTHASGLMAASSESVGCTKNREASYM---YMGDDDDERAG	4413
Db	3360	--GSRGLVDQNLN--EPATWNFTDDRNVWLQOKMGEAKDRNFTKLIEINGELDHND	3415
Qy	4414	KDFFRGLQSGDGVATFSSLSPSNIIKAKIADMQMPAPPAELAVGPFKMFYLYLYG	4473
Db	3416	LEMIRQTLQ-----HVASKLQHVQAKCSRLQ-----FETAGDD	3449
Qy	4474	VLV-VVRYIFGVILGLMRGPOTDEPPPEPTEBKIGQLRHRLLATQSSRHLPALPPADDT	4532
Db	3450	AFWIQENIDGIIUL-----QLQKLTQPGDDEHSLG-----PPSSC	3485
Qy	4533	QOMQVSAP--GLDITKEDNQIQVKPHESPSTSTPSSGEAEVSPDESADHTEEQ---	4586
Db	3486	GSUTESLMRQNTLTRLIN---QLTEBKNTLRISIVIKLEEL-----NRCYWHTCASRDCCS	3538
Qy	4587	-----PPSLDILLGGEQAKQOAKERBEAQAAQAAMSAI-----EAEKKAQGPAP---	4633
Db	3539	RFSEIDPADIEAIIASEKEVWNEKLSLQAKRAEKVYKLAELRNDALLRNLGPDTD	3598
Qy	4634	-SALSQVDLSQYTR--RAVSFLARNFNLKYVALVL	4666
Db	3599	HAALOKI-----YNYKLRASSFRKALIIYQKYLLILL	3630

RESULT 10  
US-11-070-573-68  
; Sequence 68, Application US/11070573  
; Publication No. US20060168683A1  
; GENERAL INFORMATION:  
; APPLICANT: Hey, Timothy  
; APPLICANT: Cai, Charles  
; APPLICANT: Meade, Thomas  
; APPLICANT: Moon, Haley  
; APPLICANT: Burton, Stephanie  
; APPLICANT: Sheets, Joel  
; APPLICANT: Merlo, Donald  
; APPLICANT: Wootsley, Aaron  
; TITLE OF INVENTION: Insecticidal Toxin Complex Fusion Proteins  
; FILE REFERENCE: DAS-118XC1  
; CURRENT APPLICATION NUMBER: US/11/070,573  
; CURRENT FILING DATE: 2005-03-02  
; PRIOR APPLICATION NUMBER: 60/549,502  
; PRIOR FILING DATE: 2004-03-02  
; PRIOR APPLICATION NUMBER: 60/549,516  
; PRIOR FILING DATE: 2004-03-02







Db 3384 NWEAGLSQQOATLADYTAERLSVLCNWFANLQPEGVSLSHRDDLYSFLINDQVSSA 3443  
Qy 4172 IGQKWDVLBSASNVILKLYFDMFLKLDLTSSASQEI DANNDGQVLPKDPKRWQ 4231  
Db 3444 I---KTTRLABAIAGIQLYI-----NRALNRIEPNARDVSRQFFDTWTV 3486  
Qy 4232 QKSYTPEIEFLACCETHHOGKLDYIGCDRPFHEPAKEIGFN--LAVLLTNLSEHPNE 4289  
Db 3487 NNRVY-----STWGGVSRVLYPENYIDPTQIGQTRMDELLENIS-----Q 3528  
Qy 4290 PRLARFLETAGSVLNYFPFPLGRLEIMGGSKRIERVYFEIKESNIEQWPKQIKESKRAF 4349  
Db 3529 SKLSR-----DTVEDAFKTYLTRTETVADLVKVSAYHDNVNSNTGLTFWFGQTRNLPEY 3583  
Qy 4350 FYSIV---TEGGD-----KE--KLEAFVNFCEDAI 4374  
Db 3584 YWCNVDISRMQAGELAAANAKWTKIDTAVNPKDAI 3620

RESULT 11  
US-11-056-355B-86482  
; Sequence 86482, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056.355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 86482  
; LENGTH: 1703  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(1703)  
; OTHER INFORMATION: Ceres Seq. ID no. 12690877  
US-11-056-355B-86482

Query Match 0.8%; Score 219; DB 7; Length 1703;  
Best Local Similarity 18.9%; Pred. No. 0.00031;  
Matches 273; Conservative 246; Mismatches 481; Indels 446; Gaps 69;

Qy 3083 NKLLKPSSTTFSRRSSFKTSTR-----DIKFFSKAVLPMLMEKYFSTHRNYFIAVAT 3133  
Db 121 NIAFMEDPQSVSSGKGFTAKARKGLNFNNVDGKEINAKVLSER-ASKAEABIVALKD 179  
Qy 3134 ATNVVGAASLKEKEMVAALF---CKLASLSRLAAGFDPVRIIVRCLQVLVKIGDAKSL 3190  
Db 180 ALSKVQA-----EKEASLQAQFQNLKUNLSESVRAQEDSRVLIE-----RATRAEAE 229  
Qy 3191 VKNCPEFI-----RTSMLTF--FNNVADVVGHTIMNLQDGKYAHLGRTHLXTSTSLG 3240  
Db 230 VETLRESLSKVEKESLSLQYQQCLQNIAD-----LEDRLSLA 268  
Qy 3241 YINGVLLPILPAKFDHLANCYEGADLLDEITQVASYKMLGSLYALGTADSTHDPKYLKT 3300  
Db 269 QKE-----AGEVDERANRAEAETLALKQSLVSS-----ETDKEAALVQYQQCLKT 313  
Qy 3301 EIERHKPALGSLGAFSFTFPVAFLEPHLNKHNFSLNRIADLSLEAQDIMQWQECMP 3360  
Db 314 -----ISNLEERLHKAEDSRLTN-----QRAENAG 340  
Qy 3361 TLETILGEVDQFVSDKTYN--EAPHIIDVILPLCLSYLPFWMAQG-----PDNVTP 3410  
Db 341 EVESLKKQVSKLIENEAYELQYQQCLDTIADL---KLKLPHAQEETQRLSREIEDGVAK 397

Qy 3411 TGCNHTVMTVAEHMOLLKNVLKLIKNIIGNENAPWMTRIATVYTOQIIINSSEBELLRDSF 3470  
Db 398 LKFAEBKCVVLSRNQNLHSELGLLEKLGNO-----SHELTEK-- 436  
Qy 3471 LPLAERVRKRTDMNFH--KEESLRGFIKST--DDTSQVESQIQEDMQLLVRDIYSYPL 3526  
Db 437 -----QKELGRLWTCVQENLR-FWEABTAFTQLQHLHSQSEBELSTLLELQNRSQI 488  
Qy 3527 LIKYVDLQ--RNHWLRNVPABEALYHNVHAIFNWKSQYFLKEEQNFISAN-----EI 3579  
Db 489 L---KQMEARNLNQBEVQEAQKQSLNELNLSAASIKSLQBEVSKLRETIOKLBAEV 545  
Qy 3580 DNMVIMPTATRVATVTDGTPQGGKKKKKRRDKRDKDKEVQASLWMAVLKRLLPVGL 3639  
Db 546 ELRVDORNALQOBIYCLKEELSQIG-----KKHQ-----SMVEQVELVGL 585  
Qy 3640 N--LFAGREQELVQHCKDRFLKXMSQDVAEFAKTQTLTPDKIDPADEMSQHYLSKLG 3697  
Db 586 HPESFGSSVKELQE--ENSKLKEIRERESIE--KTALI--EKLEMEKLVQKNLLE--N 637  
Qy 3698 SKSKSNITVETAKIIDDVTVERIVAMSKVLFGLH-----MIDHPQQMSKN----- 3745  
Db 638 SISDLNAELETIRGKLKTLB---EASMSLAEEKSLHSEKMDLISRLQASATENSUKLSEE 694  
Qy 3746 -----VYRSVVSIOKRAVIACFRQTSLSLSPRHACNIFARTYYELWLEENIQEV 3798  
Db 695 NMVLENSLFNANVELEBK-----SKLKSU--BESCHLLNDDKTLTISERESLSHI 744  
Qy 3799 -----MIEDITQSFEDEALKKSDVBEGEKPDLTQTLVTTFCRGAMTERSGALQE--DPLY 3852  
Db 745 DTKRKRIEDLEK--EHAELKVK-VLE-----LATERESSLQKIBELG 783  
Qy 3853 MSVAHIIAKSCGEEBEGGEEBEGGEEA---FAEDEGRASIIHEQMEKOKLFLPHQARLA 3909  
Db 784 VS---LNAKDCYASVFQFSESRRMNGMESTIHLQDENQCRVREYQVELDRA--HDAHI-- 837  
Qy 3910 DRGVAEMVLLHISASKGLPSEMVKTLQGI---SILRGNNIDIQMG--MLNHL---KDK 3961  
Db 838 -----EIIVL-----QKLDWLKSSSLIAENQDIKESKLEKLVLSLEE 879  
Qy 3962 KDVGFSTIAGLNSCSVLDDAFERNTKAE---GLGVGLEGAAGEKNMHDABFTCALFR 4018  
Db 880 ENIGKQVQIDSSINCILKILRTGIYQVLMKLEIIPGIGSGDENSQRDQNMHD-----ILN 933  
Qy 4019 FIOLTCEGHNLDWQNYL---RTOAGNTTTVNVICTVDYLLRLQESIMDYPWHYSKELI 4075  
Db 934 RLE-----DMQTMLLSIRDENQHSATENLVL---IEFLRLKLS----- 968  
Qy 4076 DPAGKANFFKAIGVASQVFNLTTEVIQGPCTQOQALAHSLRLWDVAGGFLPLFSHMQDKL 4135  
Db 969 -----EAVGIETEK-KILEEBEESQC---QQLSFSR--DETQKLIFFVNGELTKV 1012  
Qy 4136 SKHSSQVDDL-----KELLNLQKDMIPMLSMLEGNVYVNGTIGQMVDTLVESASNV 4187  
Db 1013 NOGVNREKVLWVEIEDFHRQVQLRDDY-----TILQDGNK 1049  
Qy 4188 ELILKVPDMLKLDLTSSASQEI DANNDGWLVPKDPFKEMEQOKSYTPEEFILACC 4247  
Db 1050 TLDEKAY-----LTKSTL-----QLEEEKCKLEDISLLLS-- 1080  
Qy 4248 ETNHDGKLDYIGCDFRPFHEPAKEIGFNLA VLLTNLSEHPNEPRLARFLTAGSVLVNFE 4307  
Db 1081 ETIYQS-----NLIITLSEDV-----ILEKLSGAMKLINE 1108  
Qy 4308 PFLGRIEIMGG--SKRIERYVFEIKESNIEQWPKQIKESKRAFFYSI----- 4953  
Db 1109 D-LDRLSIVKCLKEEVRELGDKLSADIANFOLQVVLEKSNALLESARGANVHLEHEIA 1167  
Qy 4354 -VTEGDDKEKLEA--FWNFCEDAIPEWTHA--SGLMAASESVGCTKNREASYMVGDDDD 4409  
Db 1168 NVKVOKEKELAMLAMTISIMQNEKSELSKAVEGLECRYEKAIEEDRDQVLRLRGDYD 1227  
Qy 4410 ERAGKD 4415



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; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 86480
; LENGTH: 1744
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(1744)
; OTHER INFORMATION: Ceres Seq. ID no. 12690875
US-11-056-355B-86480

Query Match      0.8%; Score 219; DB 7; Length 1744;
Best Local Similarity 18.4%; Pred. No. 0.00032;
Matches 273; Conservative 246; Mismatches 481; Indels 446; Gaps 69;

Qy 3083 NMKLLKPTTFSRRSSFKTSTR-----DIKFFSKAVLPLMEKYFSTHRNFIYAVAT 3133
Db 162 NIAFMEDPQSVSSGKGFATARKGLNPNVVDGKEINAKVLSER-ASKAEAEIVAKD 220
Qy 3134 ATNNVGAASLKEKEMVAALF---CKLASLLRSRLAFAFGPDVRIIVRCLQVLVKGIDAKSL 3190
Db 221 ALSKVQA-----EKEASLAQFQNLKLSNLESEVSRAQEDSRVLE-----RATRAEAE 270
Qy 3191 VNCPEFT-----RTSMLTF---FNNVADVGHITMNLQDGKYAHLRGLTKTSTSLG 3240
Db 271 VETLRESLSKVEKESLSLQYQCLQNIAD-----LEDRI SLA 309
Qy 3241 YINGVLLPILTAKFPHLANCEYAGADLLDELQVASYKMLGSLYALGTDAISLTHDRKYLKT 3300
Db 310 QKE-----AGEVDERANRAEAEATLAKQLSVSS-----ETDKAAALVQYQCLKT 354
Qy 3301 EIERHKPALGCLGAFSTFPVAFLEPHLNKHNFSLNRIADHLSLEAQDITMQWEQCMF 3360
Db 355 -----ISNLEERLHKAEDSRLTN-----QRAENAE 381
Qy 3361 TLETILGEVDQFVSDKTYN-EAPHIDVLPILCSVLPFWMAQG-----PDNVT 3410
Db 382 EVESLQKQVSLIBENEAYELQYQCLDTIADL---KLKLPHAQEETQRLSREIEDGVAK 438
Qy 3411 TGGNHVTMTVAEHMNLKLVLLKIKKNIGNENAPWMTRIATYQQIINSSELLRDSF 3470
Db 439 LKFAEKCVCULERNQNHLSELDGLEKLGQ-----SHELTEK-- 477
Qy 3471 LPLAERVKRKTDMFPH--KEESLRGFIKSST--DSTSQVESQIQEDWQLLVRIYFYPL 3526
Db 478 -----QKELGRLWTCVQENLR-FWEAEATFQTLQQLHQSQDEELSTLALQLNRSQI 529
Qy 3527 LIKYVDLQ-RNHWLRNNVPRAEELYNHVAEFTNWSKSYPLKEEQNFISAN-----EI 3579
Db 530 L---KDMERNNGLOEEVQEAQDQSKSLNELNLSAASIKSLQSEVSKLRETIQKLEAEV 586
Qy 3580 DNMVLIPTARTVATVDGTPOGGKKKKKGRDKRDKKQVQASLMVACLKELLVGL 3639
Db 587 ELRVDQRNALQOETCYCLKEELSQTG---KKGQ-----SMVEQVELVGL 626
Qy 3640 N--LPAGREQELVQHCDFRFLKMSQDVAEFAFKTQLTPKIDPADMSMQHLYSLKLG 3697
Db 627 HPESFGSVKELQE--ENSKLKEIRERESIE--KTALI--EKLEWMEKLVQKNLLE--N 678
Qy 3698 SKSKSNITVETAEAKAKIIDTVIRIVAMSKVLFGH-----MIDHPQQMSKN----- 3745
Db 679 SISDLNAELETIRGLKLTLE---EASMSLAEEKSLGHSEKMDMLISRLQSATENSXKLSEE 735
Qy 3746 -----VYRSVSTQKRAVIACFRQTSLSLPHRACNIFARTYYELWLEENIGQEV 3798
Db 736 NMVLENSLFNANVEELK-----SKLSL--EESCHULNDKTKTLTSESLSLSHI 785
Qy 3799 ----MIDLTQSPEDAECLKSDVVEGEKPDPLTQLVTTFCRGAMTERSGALQE--DPLY 3852
Db 786 DTMKRRIEDLEK--EHAELKYK-VLE-----LATRESSLQKIEELG 824
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Qy 3853 MSVAHIIIAKSCGEEEBEGGEGGEA---BAEDEGRASIIHEQEMEKOKLLFPHOARLA 3909
Db 825 VS---LNAKDCFYASVQFSESRMNGWESIHHLODENQCRVREYQVELDRA--HDAHI- 878
Qy 3910 DRGVAEMVLLHISASKGLPSEMYMKTQLGI---SILRGGNIDIQMG--MLNHL---KDK 3961
Db 879 -----EIIVL-----QKCLQDWLEKSSSLIAENQDIKEASKLLEKLVSELEE 920
Qy 3962 KOVGFTSTAGLMNCSVLDLDAFERNTKAE---GLGVGLEGAAGEKMMHDAEFTCALFR 4018
Db 921 ENICKQVQIDSSINCILRTGIYQVLMKLEIIPGIGSGDENSRRDQNMHD-----ILN 974
Qy 4019 FIQLTCEGHNLDWQNYL---RTOAGNTTTVVVICTVDYLLRLQESIMDFVWHYSSKELI 4075
Db 975 RLK-----DMQTMLLSTRDENQHSAINLVL---IEFLRQLKS----- 1009
Qy 4076 DPAGKANFFKAIGVASQVFNLTTEVIQGPCTONQQAALAHSLRDWAVGGFLFLFSHMQDKL 4135
Db 1010 -----EAVGIETEK-KILBEELESQC---QQLSPSR--DETOKLIFVNGELTTKV 1053
Qy 4136 SKHSSQVDLL-----KELLNLQKDMIPMLMSLEGNVVNGTIGQMVDTLVESASNV 4187
Db 1054 NOGVNREKVLWVEIEDFHRQVLQLRDDY-----TILQSDNNK 1090
Qy 4188 ELTLKYDFMFLKLKDLTSSASFQEI DANNDGWVLPKDPKKEKMEQOKSYTPEEIEFILACC 4247
Db 1091 TLDEKAY-----ITKSTL-----QLEEKCKLEDDISLLLS-- 1121
Qy 4248 ETNHDGKLDYIGFCDFRHPHEPAIGFNLAIVLLTNLSHMPNEPLARFLETAGSVLNYFE 4307
Db 1122 ETIYQS-----NLIILEDV-----ILEKLSGAMKLINE 1149
Qy 4308 PFIGRIEIMGG--SKRIERVVFEIKSNIBQWEKPKQIKSKRAFFYSI----- 4353
Db 1150 D-LDRLSIVKVKLEEEVRELGDKLKSADIANFOLQVVVLEKSNABELLSARSANVHLEHIA 1208
Qy 4354 -VTEGGDKKLEA--FWNFCEDAI FEMTHA-SGLMAASEESVGGTKNREASVYVMGDDDD 4409
Db 1209 NVKQVQEKLELEAMLMISIMQNEKSELKAVEGLECRYEKAIEEDRDQVLRGRDYD 1268
Qy 4410 ERAGKD 4415
Db 1269 EQVKKN 1274

RESULT 14
US-10-953-349-9275
; Sequence 9275, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9275
; LENGTH: 3429
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9275

Query Match      0.8%; Score 208.5; DB 6; Length 3429;
Best Local Similarity 18.4%; Pred. No. 0.0051;
Matches 332; Conservative 246; Mismatches 628; Indels 601; Gaps 77;

Qy 1060 TGSCHALLLEASKQKQADPRTYRAEKYAVSSGKTYFEFEILTAGPMRVGWAHADMAPG 1119
Db 1865 TVETHKAEDSGSLKQKQALYNLSKADK--LVSDIPHVPDGLTTTSGSV---ANKQVDIG 1918
Qy 1120 MMLQGDENSWAFDGYNEEKYVSGNTESFGKQWAGDVGVGVFLDLIDTISFSLNGELMD 1179
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Db 1919 SSKVAENELV-----KIPGDDVSSVQLSLGNTLTAKSSL-EKCTADQLLEKLSQ 1970  
Qy 1180 ALGGTTTFADVGDNFVACTLGVQKARLTGVQDVTNLTLYFTTCGLQBGVEYPPFCVM-- 1237  
Db 1971 E--GETTPAS-DGE-----TCHLAETASLSVVRSEPTASATTA-----EPLFTDKLE 2017  
Qy 1238 -----KRDVTHYTKDQ-----PIFENTDEMIDTRIDVTRIPAGSDTPPC 1277  
Db 2018 KNISFQDEVKTLNGDKREAILLSSEEQTNVNSKIETNSELOASRTD----- 2064  
Qy 1278 LKISNHTFTMKANWEFLURLSLPVICHNEFTDEAKARRWEIIRDOQILMKEAVEAQM 1337  
Db 2065 -EVPHVDSKSDVA-----NQTVKE-DEAKHSEI-----QSSMLE----- 2098  
Qy 1338 PAHIDIMRSGFTMDIKGLHYE-----DNQEELPSSKMKRLPSRPPKSGMTRGV 1388  
Db 2099 PDELNPAGQKHSSIDLQPLVLVTNENAMSLDDXDYDPIKSADIQDP-----ESV 2152  
Qy 1389 TIQYNNLNQGVNGMHRSTSEA-----EMAKYDLGAQGLTPDDKDKRGRSPFKPF 1440  
Db 2153 FVQGVGRPKVGTADTQMETNDNAKLLVGCSESEKEKTLQSLIPGDDADTE-QDPEESV 2211  
Qy 1441 RSKRG-----ESSDRASRKSKTDPDPFSDTEVSPE-----RG 1472  
Db 2212 SDQRPKVSAYTQMEDTDEAKLLMGCSVESEKEKTLQSHIPGDDADTEKNPEESVSQG 2271  
Qy 1473 ARBPPOIKVQANQRYNGWNPASRTNLYGQVGLNMPATPDQRKQMTTSLAQSATET 1532  
Db 2272 VDRP-----KVGTTDTQME-----DTNDAKLLVGCSESEKEK 2305  
Qy 1533 VGNEIFDAECLLINEFYGVRIYPCQDPTHVVGWVITQYHLHSDFNQSKVTKSSVII 1592  
Db 2306 -----TLQSHIPGDDADTEQNPESVSU 2328  
Qy 1593 TDDYDRVENVARQSCYMRADLYNEVMAEATAGASQGMFIGCSVDTS----- 1642  
Db 2329 QGVNRPKVGNTQ--MEDTDE-----AK-----VLVGCSESEKEKTLQSHI 2370  
Qy 1643 -----TGSVFTCEGKDTSPFKWE--PETKLPAIFVETASKELIQLIELGRSA 1689  
Db 2371 PGDDADTEQNPESVSFNDPRDKGTADTHMEDIDDAKLLVGCSESEKE----- 2420  
Qy 1690 TSLPLSAAVLPTSDKHVIFQFPRLKVQCLKQHWARVPNQSLQVHA--LKLSDIRGWSM 1747  
Db 2421 -----KSLQSH-----MPSDDAVLHAPFENTKDSKGDLL 2449  
Qy 1748 LCEDAVSMLALHIPER-----DRCIDIILEPIEMDKLLSFHSHTLTYAA 1791  
Db 2450 HGESLVSCPTMEVMEQKGFETHARTDSGGIDRGNEVSENNSDGVKMNISVQVP--- 2505  
Qy 1792 LCYQSNYRAHALCTHVDQK--LLVAIOSQM-----SGPLRGFYDLLIALHLESH 1842  
Db 2506 -----DASHDLNVSQDQTDIPLVGGIDPHEVQNVDPASP--HGAAPNIVIFQSEGH 2556  
Qy 1843 -----ATTMEACKNEFVPLPGLKALVEEPMGHSLSRLSTESVRPOMKMTDTA 1892  
Db 2557 LPSFILPDDVAGLESNSNDEKTNISSE-----QVPDVSHDLKVSDQDQTDIPVGGI-VP 2610  
Qy 1893 ESITISNLYSPFPFLEAVREFVQALAEAVETNQVHNRDPVGCSENENFLPLIKLIVDLR 1952  
Db 2611 ENLQEIADV--PASPHGVVPDVV-----SQSEETQSPSILPDD-- 2647  
Qy 1953 LLVGMMDREDEKLLIM-----TNPETWDPFDEKGDHRRKGLLHMKMAE----- 1998  
Db 2648 -VPGQPDGNCCKMDTWQNNTSIDIGTSKTCQPSSTQCPEDENRNSLSHCPEPSVVEQ 2706  
Qy 1999 -GAKLQWCYLLQHLNDIQLHRVREAIAPAFHDFVGLQDQ-----LRYTETIKQSDLS 2052  
Db 2707 RQSRDQVC-----IGSVE--SQVEISSAILENRSADIQPPQSILVDQKDIESKEPGIES 2759  
Qy 2053 A-VAACKTREFRCPPR---EQMNAISLFXHLEEDKENCPCGBELIARMEFHDITLMAHV 2108

Db 2760 ADVSLHQLADIQAEPNSLVDMQDI-----ESKE-----PGTESADV 2796  
Qy 2109 SLHAL-----QEPDAENQEP-----EAKPGAFGLKLYNIINTVKEL 2144  
Db 2797 SLHQLADIQPGSILVDQMDTEKSKPEGTESADVSLHQLADIQGP-SILVDQMDTEKSK 2855  
Qy 2145 EEEAKAIBEPKPKTPEEKFRKVLQTIWNWAEESQIETPKLVREMFSLVRYQDAVGELI 2204  
Db 2856 EPAVKQNTEDKQSHVETAGSELVDVSAECSTEQVOLPPSPVGMHVLHGLASKSEIV 2915  
Qy 2205 -----RALEKTYVINAKTKLDVAEMVMVGLSOTRALLPVQM-----SQBE 2243  
Db 2916 AEGTDFSSLPKTEENAKSQLADTEPSSSLTAQVKNIEDQVETAGCFVWVSTCGSTEP 2975  
Qy 2244 BELMRKLWLKLVNNHTFFQHPDLIRLVLRVHENVMAVMNTLGRRAQAQSDAQSPSQVA- 2302  
Db 2976 QVOLPPSAEPVVAEGTEPSSLLMTGVDNSSLMTGVDNAKTHLA---DVPVSSSPTTM 3031  
Qy 2303 EDSKEKOTSHEMVWVACCRFLCYFCRTGRQONKAMPDFDFFLENSNILLRPSLR---GS 2359  
Db 3032 EKNTEAQDQDQVTTGGCGLV-----DVLTECS---SEPQLQPPSA 3069  
Qy 2360 TPLDVAYSSLMNTELA-LALREHYLEKIAVYLSRCGLQSNSELVEKGYDGLWDPV--- 2415  
Db 3070 EPV-----ISEGTBLATLPLTEE--ENADSQLANIEPSSPVVVEKNIEAQDQVKTA 3121  
Qy 2416 -----EGERYLDFLRCVWYNGESVEENANLVIRLLIRRPCC 2452  
Db 3122 GCELVSTGCSSEPPQVHLPPSAEPDGD-----IHVHLKETEKSESNV- 3163  
Qy 2453 LGPALRGEGELLLKA--IVDANKMSERIADRRKUREMEQEGDVNFSPH--LPSEDEDEDY 2508  
Db 3164 -----VGEGTAPPSPPLVTEGNAESQLADTEP-----FTSPVVEKNIKDQSQ 3207  
Qy 2509 IDTGAAILNFYCTLDLLGRCAPDAGVIALGKNESLRARALSLRVLV-LEDIQGVLSLRF 2567  
Db 3208 VETTG-----CGLVDDSTGCSSEPPQV-----QLPPSAEPMEGCGDL--- 3243  
Qy 2568 TLNPPAAGEERPKSDMPGLIPGHRQSVGLFLERYVGIETBELFYKLLEAEFLPOLRAAT 2627  
Db 3244 -INVPSGCGSTEQIQLSSAEP--EGMHILHEAMNSET-----VVTGSELPSLSPMT 3295  
Qy 2628 MLDRNDG 2634  
Db 3296 EDENADG 3302

RESULT 15

US-10-953-349-9274  
; Sequence 9274, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 9274  
; LENGTH: 3438  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-9274

Query Match 0.8%; Score 208.5; DB 6; Length 3438;  
Best Local Similarity 18.4%; Pred. No. 0.0051;  
Matches 332; Conservative 246; Mismatches 628; Indels 601; Gaps 77;  
Qy 1060 TGEQHEALLLEASKQKQADFRTYRAKNYAVSSGKWFYFEFILLTAGPMRVGWAHADMAPC 1119  
Db 1874 TVETHKAEDSSGLKNQKALYNLSKADK--LVSDIHPHPVPGDLTTSQSV-----ANKQDVIG 1927



Qy	1120	MMLGQDENSNAFDGYNBEKVYSGNTESGFKQMAVGVDVGVFLDLIDKTIISFSLNGELMD	1179
Db	1928	SSKVAENELV-----KIPGGDVDSVQLSLGNTLAKSSL-EKCTADQLLGEKLSQ	1979
Qy	1180	ALGETTFADVQGNFNPACTLGVQKARLTYGDVNTLKYFTTCGLOGEYGEFFCVNM--	1237
Db	1980	E--GETTPAS--DGE-----TCHLAETASISSYRSEPTASASTA-----EPLTDKLE	2026
Qy	1238	-----KRDVTHWYTKQ-----PIFENTBEMIDTRIDVTRIPAGSDTPPC	1277
Db	2027	KNISFQDEVKTLNGDKKEAIIILSSEEQTVNNSKLEINSEELQASRTD-----	2073
Qy	1278	LKISHNTFETMEKANWFLRLSLPVI CHNFEI DBAEKARRWEIFKORQQLMKEAVEAQM	1337
Db	2074	-EVPHVKGKSDVA-----NQTVKE-DEAKHSVEI-----QSSMLE-----	2107
Qy	1338	PAHIDQIMRSGFTMNDIKGLHYE-----DNQEBELPSSKMKLPSRPRKGSMTRGV	1388
Db	2108	PDELPNAGQKHSHSIDLOPLVLTNSNENAMSLDDKQYDPIKSKADIQBDP-----EESV	2161
Qy	1389	TIQYNNNLQPCVNGMHRSTSEA-----EMAKYDLGAQGLTPDDBKKGRSPFKFF	1440
Db	2162	FVQGVGRPKVGTATQMEDINDAKLLVGCSESEKEKTLQSLPGDDADTE-QDPEESV	2220
Qy	1441	RSKRG-----ESDRAKRSKSTPPDPFSSTVESPE-----RG	1472
Db	2221	SDQRPKVGSAYTQMEDTDEAKLLMGCSESEKEKTLQSHIPGDDADTEKNPEESVSQ	2280
Qy	1473	ARRPNQIKYSOANQRNGYNMARSRTNLVGSQVGLNMAPTDQRKOMTSTTIAQSATET	1532
Db	2281	VDRP-----KVGTDTQME-----DTNDAKLLVGCSEVASEKEK	2314
Qy	1533	VGNEIFDAECLKLINEFYGVRIYPGQDPTHVIGWYTTQYHLHSKDFNOSKVTKSSVII	1592
Db	2315	-----TLQSHIPGDDADTEQNPPEESVS	2337
Qy	1593	TDDVDRVVENNRQSCYMRADELYNEVMAEATAKASQGMFTGCSVDTS-----	1642
Db	2338	QGVNRPKVGNANTQ--MEDTDE-----AK-----VLVGCSESEKEKTLQSHI	2379
Qy	1643	-----TGSVSTFCGKOTSPFKFME--PETKLPPAIFVEATSKELIQLGRSA	1689
Db	2380	PGDDADTEQNPPEESVSFNDRPKOGTADTHMEDIDDAKLLVGCSESEKEK	2429
Qy	1690	TSLPLSAAVLFTSDKHVIPPQPPRLKVQCLPQHMARVPNQSLQVHA--LKLSDIRGWSM	1747
Db	2430	-----KSLQSH-----MPSDDAVLHAPPENTKDSKGGDL	2458
Qy	1748	LCEDAVSMLALHIFEE-----DECIDILEPIEMDKLLSPHSHTLTLYAA	1791
Db	2459	HGESLVSCPTMEVMEQKGFSETHARTDSGIDRGNEVSNMDSGVKONTSSVQVP----	2514
Qy	1792	LCYQSNYRAAHALCTHYDQKQ--LLYAIQSOYM-----SGPLRQCFYDLLIALHLESH	1842
Db	2515	-----DASHDLNVSQDQTDIPLVGGIDPEHQENVDPVPS--HGAAPNIVIFQSEGH	2565
Qy	1843	-----ATTWEACKNEFVIFLGPPELKALVEEPMGHSLRSLOTESVVRPOKMTDIA	1892
Db	2566	LSPSILPDDVAGQLESMSNDEKTNISSE-----QVPDVSHDLKVSOQDTDIPPVGGI-VP	2619
Qy	1893	ESITEINLVSYPPELVAREFVMOALAEAVETNOVHNRPVGGSENFLPLIKLVDRL	1952
Db	2620	ENLQEIYDV--PASPHGVVPDWW-----SQSEIQSPSILPDD--	2656
Qy	1953	LLVGMRDEDEVKLLIM-----TNPETWDPSPDKGDKHRKGLLHMMAE----	1998
Db	2657	-VPCQPDGCEKMDTQNNNTSIDIGTSGTKCPSPSSTQPEDNRNLSLHCFSEVVEQ	2715
Qy	1999	-GAKLQWCYLLQHLNDIQLRHRVEAIIAFHADVFVDLQTOQ-----LRRVTEIKQSDLPS	2052
Db	2716	RDSRDQVC-----IGSVE--SQVRISAILENRGAIQPPQSILVADQKDIIESEKEGIES	2768

Qy	2053	A-VAAKTREFRCPPR	---EOMNAIISFKHLBEEDKENCPCGGEELIARNVEFHTLMAHV	2100
Db	2769	ADVSLHQLADIQAEP	SNLVQMDI-----EESKE-----	2805
Qy	2109	SLHAL-----	QEPDAAENOB-----EAKPGAFLKLYNIINTVKEL	2144
Db	2806	SLHQLADIQPGSILV	QMDMTKESKEPGTASADVSLHQLADIQPG-SILVQMDMTKESK	2864
Qy	2145	EEBAKAIIEPPKKTPEK	FRKVLIIQTIIVNAEBSQIETPKLVREMPSSLVROVDVAGELI	2204
Db	2865	EPAVQKNIEDKQSHVETA	GSSELVDVSAECSTEPQVLPSPSEPGVPMHVLHGASKSEIV	2924
Qy	2205	-----	RALEKTVVNAIKLVDVAMWGLSGIQRALLPVQM-----SQSE	2243
Db	2925	AEGTDFSSSLPKTEB	ENAKSQALADTEPSSSLTAVQKNIEDQVETACCFVWVSTGCTSTEP	2984
Qy	2244	BEMLKRLMKLVNHNTH	FFQHPDLIRVLRVHENVMAVMNTLGRRAQAQSDAQPSSOPVA-	2302
Db	2985	QVQLPPSAEPVAEGTE	FPSSLLMTGVDNSHLMTGVDNAKTHLA-----DVVPSSSPTTM	3040
Qy	2303	EDSKERDTSHEMVVA	CCRFLCYFCRTGRQNOKAMFDHDFLLENSNILLRSLSR---	CS 2359
Db	3041	EKNIEAQDQDVTTGG	CGLV-----DVLTECS-----SEFQLQPPSA	3078
Qy	2360	TPLDVAYSIIEMENTLA	-LALREHYLEKIAVYLSRGLQSNSELVEKYPDLGWDVPV---	2415
Db	3079	EPV-----	ISETGELATLPLEE--ENADSQLANIEPSSPSVVEKNTIEAQDQOVKTA	3130
Qy	2416	-----	EGERYLDLFRFCVWNGESVEENANLIVIRLLIRRPPEC	2452
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Db	3305	EDENADG	3311	

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Job time : 164 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: October 10, 2006, 15:44:08 ; Search time 854 Seconds  
(without alignments)  
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Perfect score: 5000  
Sequence: 1 ctgaattcggaattcccatc.....ggtgaccaccagctaccact 5000  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1403666 seqs, 935554401 residues  
Total number of hits satisfying chosen parameters: 2807332  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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				2: /EMC Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*	
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				10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles.seq:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	869.4	17.4	15378	3	US-08-785-420-1 Sequence 1, Appli
2	840.8	16.8	4078	3	US-09-016-434-1154 Sequence 1154, Ap
3	809	16.2	15572	3	US-09-424-783-1 Sequence 1, Appli
4	65.6	1.3	1050	2	US-08-480-481-4 Sequence 4, Appli
5	64	1.3	1050	2	US-08-480-481-3 Sequence 3, Appli
6	53.6	1.1	1598	3	US-08-785-420-3 Sequence 3, Appli
7	51.6	1.0	7218	2	US-08-232-463-14 Sequence 14, Appli
8	51	1.0	900	2	US-08-480-481-6 Sequence 6, Appli
9	40.8	0.8	1334	3	US-09-668-097A-35 Sequence 35, Appli
10	39.4	0.8	294	3	US-09-252-991A-11838 Sequence 13, Appl
11	38.6	0.8	1768	3	US-09-485-529-13 Sequence 13, Appl
12	38.6	0.8	2125	3	US-09-485-529-14 Sequence 14, Appl
13	38.2	0.8	1290	3	US-09-902-540-5006 Sequence 5006, Ap
14	38.2	0.8	12950	3	US-09-902-540-1036 Sequence 1036, Ap
15	37.6	0.8	399	3	US-09-621-976-8976 Sequence 8976, Ap
16	37.6	0.8	1738	3	US-10-164-595-31 Sequence 31, Appl
17	37.2	0.7	34534	3	US-09-949-016-15141 Sequence 15141, A
18	37	0.7	474	3	US-09-621-976-18033 Sequence 18033, A
19	36.8	0.7	711	5	US-09-974-300-310 Sequence 310, App
20	36.8	0.7	1599	3	US-09-902-540-8406 Sequence 8406, Ap
21	36.8	0.7	7581	3	US-09-902-540-882 Sequence 882, App
22	36.6	0.7	1750	3	US-10-104-047-1424 Sequence 1424, Ap
23	36.4	0.7	650	3	US-09-533-559-306 Sequence 306, App

Sequence 160, App  
Sequence 15, Appli  
Sequence 14999, A  
Sequence 15000, A  
Sequence 6077, Ap  
Sequence 6158, Ap  
Sequence 1, Appli  
Sequence 11354, A  
Sequence 11295, A  
Sequence 11374, A  
Sequence 6576, Ap  
Sequence 464, App  
Sequence 432, App  
Sequence 14172, A  
Sequence 7810, Ap  
Sequence 22, Appl  
Sequence 7948, Ap  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 7533, Ap  
Sequence 53, Appl  
Sequence 53, Appl

ALIGNMENTS

RESULT 1  
US-08-785-420-1  
; Sequence 1, Application US/08785420  
; Patent No. 6001976  
; GENERAL INFORMATION:  
; APPLICANT: MacLennan, David H  
; APPLICANT: O'Brien, Peter J.  
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT  
; TITLE OF INVENTION: HYPERThERMIA  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte,  
; STATE: No. 6001976th Carolina 28234  
; COUNTRY: U.S.A.  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/785,420  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,388  
; FILING DATE:  
; APPLICATION NUMBER: US 08/030,159  
; FILING DATE: 15-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Layton, Jr., Samuel G.  
; REGISTRATION NUMBER: 22807  
; REFERENCE/DOCKET NUMBER: 3477-73  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 704-377-1561  
; TELEFAX: 704-334-2014  
; TELEX: 57-5102  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15378 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

:	HYPOTHETICAL:	NO
:	ANTI-SENSE:	NO
:	IMMEDIATE SOURCE:	
:	CLONE:	Porcine RVR1 Gene
:	POSITION IN GENOME:	
:	UNITS:	bp
:	US-08-785-420-1	
	Query Match	17.4%; Score 869.4; DB 3; Length 15378;
	Beat Local Similarity	55.3%; Pred. No. 4.6e-261;
	Matches 2099; Conservative	0; Mismatches 1591; Indels 105; Gaps 17;
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Db	139	GGAGGAGGGCGAAGATGAGTCCAGTTTTCTGCGGACAGACGACGAGGTGGTCTCTCGAC 198
Qy	329	TGCACGGCACAGSAGAGAGGG-----TGTGCCCTGGCTGCCGGAAGGTCTCGGC 376
Db	199	TGCAACGCTACGGTGTCTCAAGGACGACTCAAGCTCTGCTTGGCCGCGAGGGGCTTCGGC 258
Qy	377	AACCGGCACCTCTTCCTCGGAG--AAATTGCGCACAAAGAACATACCAGCCTGATCTGTCTGC 433
Db	259	AACCGCCTCTGCTTCTTGGAACCCACACAGCAAACGCCCCAGATGTGCCCCCGCATCTGGCC 318
Qy	434	CAGTGTGTGTTTGTCACTCGAACAGGCGCTTTCAGTAAGAGCTTTTACAAGSAGTTGGTTAAACA 493
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Db	375	-----GGCCAACACCGTGGAGCGCGGCGTGGAGTCATCCCAGSGCGGGGGCCATAGG 426
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Qy 2342 ACTACTGGTTATGTCCCATACCCGGGTGGTGAGAAAGTGGGAGGTAACCGGCGTGGGA 2401  
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Qy 2402 GACGACCTGTACTCGTAGCGGTTTGATGGCGCTACCTCTGGTCCGGCGGGAGGAGACC 2461  
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Qy 2762 TTCTACTTCGCAACCTGTTCGAAGCGG-----CCTTGGGTGGACCCCGCTAGTACAG 2815  
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## RESULT 2

US-09-016-434-1154  
; Sequence 1154, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4078 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1526977
; US-09-016-434-1154

Query Match 16.8%; Score 840.8; DB 3; Length 4078;
Best Local Similarity 55.0%; Pred. No. 1.7e-252; Indels 101; Gaps 19;
Matches 2105; Conservative 0; Mismatches 1622;

Qy 343 AGAGAGGCTGCTGGCTGCGGAGGCTCGGCAACCGGACCTGCTTCTCGGAGAAATAT 402
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Qy 403 TGCCGA---CAAGAACATACCGCTGATCTGTCCGACGTGTGTGTTGTCATCGAACAGGC 459
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Qy 460 GCTTTCAGTAAGCTTTACAGGAGTTGGTAAACAGCTCGCGGATCTGAACTG----- 512
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Qy 513 -----GGAAAGAAACCTTAGTAAAGGTACCGGTTCTGGTTATCTGTAC 555
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Qy 556 GCTACTATACGGCAATGCTATCTTTTTCGCAATCTTAAACAGTATGTAACCTGGCCTG 615
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 516 ACTCTCTACGGACATGCCATATTGCTGCGCATTCTCCTATAGTGGCATGTATCTGTCTG 516
Qy 616 CCTGTCAACATC---ATCATCCAGGATAGCTGGCCTTTGACGTGGTCTGCAACAGCA 672
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871 AGAACATGTTGAAGACGACGCGAGAACTGTTTATTATGAAGTGGCGCTGCTGCTGTTCA 930
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931 TGCACGTTCCCTTTGGAGACTAGAGACGCTAAGAGTTGCTGGAGTGGAGCCACATAAG 990
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991 ATGGGACAGCCATTCGACTACGCCATGTCAACAGGAAATATCTTGAATCTCATGGA 1050
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1051 AGCAAAACCTTCTACTCATGCAAAAGAGAAAGCTGATGTAATAATCAACAGCATTTAC 1110
Qy 1210 CTTGCCCAGGAGAGGATGATCAGAAAGCAAGTGTGTAAGACAGGACTTGGAGGTCTAT 1269
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1111 CTTCCGGTCTTCCAAAGGAAAAATTGGATGTAGGGGTGAGA---AAAGAAAGTAGATGCCAT 1167
Qy 1270 AGGCGGCCCATCATCAAGTACGGTCACTCCACCGTCACTTGTGCAGCATTCGGAGACTGG 1329
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1168 GGAAATCTGAAATAAAATACGGTGACTCAGTATGCTATATACAACATGTAGACACAGG 1227
Qy 1330 CTTGTGCTGCTCTTATAAGTCTTTACGAAACGAAAGAAAGGCGTGGTAAAGTAGAAGA 1389
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1228 CCTATGGCTTACTTACAGTCTGTGGACGCGTGAATCCGTGAGAATGGGATCTATACAACG 1287
Qy 1390 GAAGCAAGCGATTTCTCCAGAGGAAAGGCAAGTAGGACGATGGCTCGACCTCTCCAGGTC 1449
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1288 TAAG---GCTATTATGCATCATGAAGGCCACATGSGATGATGGCATAAAGTTTGTGAGATC 1344
Qy 1450 ACAGGAGGAGATCTATGACTGCTCGAGTTATCAGSAAAGTGTCTTTCGCTGTTTCACTAA 1509
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1345 CCAGCATGAAGAAATACGACACGCGGAGTTATCCGAGACACAGTCTTCTCTTTTCAATAG 1404
Qy 1510 GTTTATCAATGGCGCTGGAAAACCTCTTCAAGAGAAACCGTCTGCTCACTGATGTTTTCGCGTC 1569
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1405 ATTTATAAGGGGCTTGTATGCTCTCAGCAAGAAAGCAAGGCTTCCACAGTCGATTTGCC 1464
Qy 1570 AGTGAAACCTGGGGGAGATGTTGATGTTCTTGAAGATCTCACCACTATCTTTCGACAGCC 1629
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1465 TATAGAGTCG-----TAAGCCTAAGTCTGCGAGATCTCATTTGGCTACTTCCACCCCCC 1518
Qy 1630 CGATGAGGATATGGAACACGAAAGCAAAACAAATTCGCGCCCTCCGCAACCGTCA 1689
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1519 AGATGAGCATTTAGAGCATGAACAAACAGACAGACTACGAGCCCTGAAGAAATCGGCA 1578
Qy 1690 GGACCTGTTTCCAGAGAGAGGCACTACTGAACTGTGATCCTCGAAGCTATAGACAAGATCAA 1749
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1579 AATCTCTTCCAGAGAGAGGAAATGATCAACCTCGTGTGAGTGATAGACCGTTTGCA 1638
Qy 1750 CGTGTCACTGCCAGGGGTTCTGGCTGATTCCTGGCGGAGACGAAATCTGGACAGAG 1809
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1639 CGTCTACAGCAGTGCAGCACACTTTGCTGATGTTGCTGGGCGA---GAAGCAGAGAGTC 1695
Qy 1810 CTGGGAAATGATATCTGGATATTTGATCATAGTTGCTGGCGCAATAATAAAGCAACCA 1869
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1696 TTGGAAATCCATTTCTGAAATTTCTGTATGATGTTGCTGGCGGCTCTAAATAGAGAAATCG 1755
Qy 1870 CAGCAACTGGCGCAGTTCCGAACTCGAAACCGGTTCAACTGGCTGTTTCTCGGCGCTCGG 1929
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1756 TAAAAACTGTGCTCAATTTTCTGGCTC-----CCTCGACTGGTTGATCAGCAG 1803
Qy 1930 CTCGACAGGCTCGGGCGAGGCAACCGCATGCTCGAGTGTCTGCACTGCACTCTCATCGA 1989
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1804 ATTGGAAGACTGGAAGCTTCTTCAGGCATTTCTGGAAGTTTACACTGTGTTTAGTAGA 1863
Qy 1990 CTGCGCTGAAGCCCTCAATATGATGAGGAGCAACACATAAAGTGAATAATCTCTCTATT 2049
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1864 AAGTCAGAGAGCTTAAATATTAATAAGAAAGACATATAAATCTATATCTCACATTTT 1923
Qy 2050 AGAAAGACGCGGACCGACCCCTAAAGTACTAGATGTGCTATGTTTCACTCTCGCTCGGTAA 2109
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1924 AGACAAACATGGAAGAAATCAAGGTTCTGGATGTTCTGTGCTCACTCTGTGTTGCCA 1983  
1983  
2110 CGGGTTCGGTGGCTCGTCAAGAAACATCTCGGACTATTTGTCGCCGCGCAAGAA 2169  
2169  
1984 CGGGTTCGAGTCCGTTCTAAACAGACTCTCATCTGTGACAAATCTCTACAGGAAGAGA 2043  
2043  
2170 CTTGTTGCTGCAAACTCGGCTTGTAGATCAAGTATCTAGTGTCTGCTCGGAAACATCTTCGT 2229  
2229  
2044 CTTGTTATTCAGACACGCTCTTTGTGAACCATGTGAGCAGCATGAGACCAATATTTTCT 2103  
2103  
2230 GGGCGAGTGAAGAGGTGGGAGTGTACCGAAATGTTATCTCGAGGTGACTATGGACCA 2289  
2289  
2104 GGGCGTCACTGAAGGTTCTGCTCAGTAAAGAAATGTTACTATGAATTTGATGTTGGACCA 2163  
2163  
2290 CATAGAG---AAGACCACACATATGATGCCACATCTAGCATAGATGGGCTTAACACTAC 2346  
2346  
2164 CACAGAGCCCTTTGTGACAGCTGAAGCAACTCACTGCGAGTGGGCTTCCACTGA 2223  
2223  
2347 TGGTTATGTCCTCATACCCGGTGTGTGAGAGTGGGAGGTAAACGGCTGGGAGACGA 2406  
2406  
2224 AGGATATTTCTCCTTACCTTGAGGGGGGGAAGAGTGGGTGGAATGTGTGGAGTGA 2283  
2283  
2407 CTTGTACTCTGACGGGTTTGTAGCGCCCTAATCTCTGTTCCGGCGGAGGAAAGACCCGGT 2466  
2466  
2284 TCTCTCTCTATGGAATTTGATGGCTTCACTCTCTGGTCAGGTTG-----TATTGCTCG 2337  
2337  
2467 CAAATAGGACTCATGCTGAAGAGCCTTATATAGGAAGGTGACGTAGTGTGCAATT 2526  
2526  
2338 TACTGTAAAGCTCACCAAAACCAACATCTGTGTAAGAACTGATGATGTCATCAGTTGCTGTT 2397  
2397  
2527 GGACCTGACGTTACCCATCATCACTTCACTGTTCAACGGAGTGGCGGTGACGGGATCTT 2586  
2586  
2398 AGATCTGAGTGGCCCAAGCACTCTGTTTGAATTAATGACAACTGTTCAAGGAATGTT 2457  
2457  
2587 CACCAACTTCAATCTGGAAGGCACTTCTTCCGGTCACTGAGTCTCTAGTAAGCTGAG 2646  
2646  
2458 TGAGAAATTTCAACATCGATGGCTCTTCTTCCAGTCTGTAGTTCTCTGCGAGGAATAA 2517  
2517  
2647 TTGTCGGTTCGTGTCGGCGGAGAACACGGTATAGCTCGGTTAGCTCGGAAGGCTA 2706  
2706  
2518 AGTAGGCTTCTGCTTGGAGGCGCATGAGAAATTCAAATTTCTTCTCCACCTCGGTA 2577  
2577  
2707 CTCCCGCTGGTGGAGTCTCTCTCCGCGCAGAGATCTCAGCTGGAGCCGTGCG- 2761  
2761  
2578 TGCTCTTGTATGAAGTGTCTGCAAAAGAAAAGTTGAAGTGGAAACACAGCCGAGA 2637  
2637  
2762 -TTCTACTTCGGCAACCTGTCCAAGCGGCGCTTGGCTGGACCCCGCTAGTACAGGACGA 2820  
2820  
2639 GTACAGCAAGAAAGAACTTACACACGCGACCTGTGGGCCCCACAGTTTCCCTGACGCA 2697  
2697  
2821 TACGGCTTTTGGCTTACGCTGTTGATATTTTACAGATTAATCTGCTTACATATGTGGA 2880  
2880  
2698 AGCTGCTTTCACACCCATCTCTGTGGATACAGCAGACGCTGTTGCTCTCTCATCTAGA 2757  
2757  
2881 ACAATTCAGAGACAAGCTAGCTGAATAATTCAGAAATGTTGGCTATCAATAAGATCGA 2940  
2940  
2758 AAGAATAAGAGAAAACTGGCAGAGAAATTCATGAATCTGCTGGTTATGAATAAATGA 2817  
2817  
2941 AGCAGCTGGATGTAGGGGACACAGAGAAAGACTTGGCAAGATTCACCCCTGCTGCT 3000  
3000  
2818 GCTTGGCTGGAGTATGTGTCGGTTAGATGACAAACAGACAAACCCATGCTGCT 2877  
2877  
3001 GCGCTTTCGAGCGACTCCCGCGCTGAGAAACGATACGATATACAACTTGTGTCAGAC 3060  
3060  
2878 GGAGTTCTCAAGCTGCTGAACAGGAGCGCAATTACAACTTACAAATGTGCTTGGAGAC 2937  
2937  
3061 ACTCAAGACTATCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCTCCAGCAGC 3117  
3117  
2938 CCGTAAGACTTTGTTGGCAATTAGGATGTCATGTGGGTATATCAGATGAACATGCTGAAGA 2997  
2997  
3118 CATCCGCAACGTTCTGCTGCCCAATGAACCTTTTCATGCACTCCAGGGCTACAAGCCAGC 3177  
3177

2998 CAAGGTGAAAAAATGAAGCTACCCAAAGATTACCACTGACAACTGATACAAAGCCCTGC 3057  
3057  
3178 ACCACTCGACTGTGCTGTCACTCCCTGACACCCAAAGATGATGATGATGATGATGATGATGAT 3237  
3237  
3058 CCCTATGACCTGATTTTATCAAACTCACCCCATCGCAAGAACTATGTTGGCAAGTT 3117  
3117  
3238 GGTGAGAACACCACTTGGGTCAGGAGAGATACAGAGGATGATGATGATGATGATGATGATGAT 3297  
3297  
3118 GGCAGAAATTCATATGTTGGGCGCGGATCGAATCCGGCAGGCTGATGATGATGATGATGATGAT 3177  
3177  
3298 ACTTAATGAGACTCGGACATGATCCCGCACTCTGTCATACCCGAAAGTTGA 3357  
3357  
3178 CATCAACAGACCTAAGAACAGAAATCTCTGCTGTTTCCCTACATCTCTCTGGA 3237  
3237  
3358 CGATGCCATCAAGAAAGCCCAACAGGACACAGCCTCGGAGACTGTGAGGACCTCTGCTGAT 3417  
3417  
3238 TGACCGAACCAAGAAATCCCAACAGGACAGCCTCGGAGGCTGTGCGCAGCTGCTGCTGCTGCT 3297  
3297  
3418 CTACGGGTATATGCTGGAACCCGCTTCTGCGGAGCAGCATGAAGCACTCTTGTGGAAGC 3477  
3477  
3298 GTACGGCTACAACTTGGAAAGCACC-----AGATCAAGATCATGACGACGAGCCGAAGT 3351  
3351  
3478 GTCAAAACAGAACCAAGCCGACTTTCAGAAATACCGGCTGAGAAAGTATGCGCTCAG 3537  
3537  
3352 GTGAGCGGCAACCGGGAAGGTTCCGAATCTTCCGTGCCGAGAAAGCTATGAGTGA 3411  
3411  
3538 CTCTGGGAAGTGTGACTTTCGAGTTTGAATCTTAAACGGCTGGAATGATGAGGCTGCGCTG 3597  
3597  
3412 GCGCGGAGGTGATTTTGAATTTGAGACGGTCACTGCTGAGACATGAGGTTGGTTG 3471  
3471  
3598 GGCTCAGCTGATATGGAACCAAGAAATGATGCTCGGACAAAGCAAGCAAGCAAGCAAGCAAG 3657  
3657  
3472 GAGTCGTCTGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCTTTCGCTT 3531  
3531  
3558 TGATGTTTCAATGAGGAAAGTGTACAGCGGTAACTGAGTCTTTCGCAAGCAAGCAAG 3717  
3717  
3532 TGATGCTTCAAGGCCCAAGCGGCTGCGATTCAGGG---CAATGAACACTATGCGGCTCTTG 3588  
3588  
3718 GGTGTTGTCAGCTGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3777  
3777  
3589 CAAAGCGGCGATGCTGTTGGGCTGATGTTGATGATGATGATGATGATGATGATGATGATGATGAT 3648  
3648  
3778 ACTCAAGCGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3837  
3837  
3649 ACTGAATGTTGAATCTTCTTGTGATGATTCAGGCTCAGAACTGGCTTTCAGAGGACTTTGA 3708  
3708  
3838 GGGTGACAA---CTTTGTACCTGCTTGCACGCTTGGTGTGCGCCCAAAAGCCAGTTAAC 3894  
3894  
3709 TGTGGCGATGGAATTCATACCTGTGTGAGCTTGGAGTGGCTCAAGTGGGTGAGGATGAA 3768  
3768  
3895 ATACGGTCAGGACGTTGAACACGCTGAATACTTCAACATGTTGCTGTCAGGAGGGATA 3954  
3954  
3769 CTTTGAAGGATGTCAGACCTTGAATAATTTTACCCTGTTGCTGCTTACAGAGGGCTA 3828  
3828  
3955 TGAACCAATCTGTGTCAATATGAAGAGAGAGCTGATCTCACTGGTACACAA-AGACCAGC 4013  
4013  
3829 TGAACCAATTTGCGGTTAATACAAACAGGATATTACCCTGTTGGCTGAGCAAGAGGCTTCC 3888  
3888  
4014 CGATCTTCAGAAATACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4073  
4073  
3889 TCAGTTTCTTCAAGTTCCATCAACCATGAACA---TATAGAGGTGACCAAGATAGACG 3944  
3944  
4074 CTGTTTCAGATACACTCCATCCCTCAAGATTTCCCAACACAGTTTG 4121  
4121  
3945 GCACCATAGACAGTTTCCCATGTTTAAAGGCTCACTCAGAACTCTTTTG 3992  
3992

## RESULT 3

US-09-424-783-1  
; Sequence 1, Application US/09424783  
; Patent No. 6780608  
; GENERAL INFORMATION:  
; APPLICANT: Hakamata, Yasuhiro







## TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,481  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: UCLA012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1050 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Other  
LOCATION: 380...380  
OTHER INFORMATION: Position distinguishes idiopathic  
OTHER INFORMATION: dilated cardiomyopathy  
NAME/KEY: Other  
LOCATION: 776...776  
OTHER INFORMATION: Position distinguishes idiopathic  
OTHER INFORMATION: dilated cardiomyopathy  
NAME/KEY: Other  
LOCATION: 1...1  
OTHER INFORMATION: Position 1 corresponds to  
OTHER INFORMATION: 7987 of the rabbit cDNA homolog  
US-08-480-481-4

Query Match 1.3%; Score 65.6; DB 2; Length 1050;  
Best Local Similarity 48.2%; Pred. No. 2.8e-09;  
Matches 237; Conservative 0; Mismatches 234; Indels 21; Gaps 1;  
Qy 2828 TTGTGCTACGCTGTGATACCTTACAGATTACTCTGCTACATATGTGGACAAATC 2887  
Db 118 TTTAAACCCCAACCTGTGTGATACCTCAAAATATTAATCTCTGAGAGTTGGAAATCTTC 177  
Qy 2888 AGACAGCAAGCTAGCTGAAATATTACGAAATGTGGCTATGAATAAGATCGAAGCAGGC 2947  
Db 178 ATTAACAATAATGAGAAACATCTCTGACAAATGGTCAATGGCAAGTTAGCAATGGA 237  
Qy 2948 TGGATGTACGGCGACGAGAGAAAGACTTGCACAAAGATCCACCCCTGCTCGTCCCTTC 3007  
Db 238 TGGATTTATGAGAAATATATTACAGACTCTCCCAAGATTCAACCTTGTGATGAACCATAT 297  
Qy 3008 GAGGACTCCCGCCGCTGAGAAACGATACATATACAACTTGTGTGCGACACTCAAG 3067

Db 298 AACTATTATCTGAAAGGAAAAAATTTATCGCTGGCCAAATCAAGAATCTCTCAA 357  
Qy 3068 ACTATCTCTGGCTCTGGCTACTACAT-----CAGCTTAGATAAG 3106  
Db 358 ACTATGTGGCTTTGGGTTTGAAGAATTTGAAGAACCCTCAGAGAGACAGCATGGCCCTT 417  
Qy 3107 CTCCAGCAGCATCGCAACGTTTCGTCTGCCCAATGAACCTTTTCATGCGAGTCCAAACGGC 3166  
Db 418 TATAACCGAACTCGTGTATTTCTCAGACAAGCAGGTTTCTGTAGATGCTGCCCATGGT 477  
Qy 3167 TACAAGCCAGCACCACCTCGACCTGAGTGTGTCACTCCTGACACCCAGAGATGGATGAGCTA 3226  
Db 478 TATAGTCCCGAGCCATTGACATGAGCAATGTTTACACTATCCAGAGACCTGCAATGCTATG 537  
Qy 3227 GTAGGCCAGCTGGCTGAGAAACACCCCAACCTTTGGGCCAGGAGAGATACAGCAGGA 3286  
Db 538 GCAGAAATGATGGCTGAAACTATCATATACTATGGGCAAGAAAGAACTGGAGTTG 597  
Qy 3287 TGGACTTACGGA 3298  
Db 598 GAGCTAAAGGA 609

## RESULT 5

US-08-480-481-3  
Sequence 3, Application US/08480481  
Patent No. 5639614  
GENERAL INFORMATION:  
APPLICANT: Sen, Luyi  
APPLICANT: Philipson, Kenneth D.  
APPLICANT: Luisi, Aldons J.  
TITLE OF INVENTION: GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,481  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: UCLA012.001A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1050 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Other

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; LOCATION: 1...1
; OTHER INFORMATION: Position 1 corresponds to
; OTHER INFORMATION: 7987 of the rabbit cdna homolog
US-08-480-481-3

Query Match      1.3%; Score 64; DB 2; Length 1050;
Best Local Similarity 48.0%; Pred. No. 8.9e-09;
Matches 236; Conservative 0; Mismatches 235; Indels 21; Gaps 1;

QY 2828 TTTGTCCTACGCTGTTGATACCTTTACAGATTACTCTGCCTACATATGTGGACAAATC 2887
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118  TTTAACCCACACACCTGTTGATACCTCAAAATATTAATTCCTGAGAAAGTTGAATACTTC 177
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2888 AGAGACAAGTAGCTGAAATATTCCAGAAATGTCGGCTATGAATAAGATCAAGCAGGC 2947
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178  ATTAACAATATGAGAACATCTTCATGACAAATGGTCAATGGACAGATTAGCAATGA 237
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2948 TGGATGTACGGCGACAGAGAGAAAGCTTGCAAGATGCCACCCCTGCCTGCTGCTTC 3007
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238  TGGATTTATGGAGAAATATATTTCAGACTCCTCCAAGATTCAACCCCTTGATGAACCATAT 297
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3008 GAGCGACTCCCGCCGCTGAGAAACGATACGATATACAACTTGTGTCGACACACTCAAG 3067
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298  AAACCTATTATCTGAAAGAGAAAGAAATTTATCGTCGCCAATCAAGAATCTCTCAA 357
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3068 ACTATCTCGGCTCTGGCTACTACAT-----CAGCTTAGATAAG 3106
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358  ACTATGTTGGCTTGGGTTGGAGGATGAAAGAACCCAGAGAGACAGCATGCCCCCTT 417
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3107 CTTCCAGCAGCAGCATCCGCAACGTTCTGTCGCCAATGAACCTTTTCATGCAAGTCCAAACGC 3166
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418  TATAACCGAAGCTCGTGGTATTTCTCAGACAAGCCAGGTTTCTGTAGATGCTGCCCATGGT 477
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3167 TACAAGCCAGCAACCTGACCTGAGTGTCTGACCTGACACCCAGATGATGATGAGCTA 3226
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 478  TATAGTCCCGCAGCCATTGACATGAGCAATGTTACACTATCCAGAGACCTGCACTGCTATG 537
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3227 GTAGCCAGCTGGCTGAGAACACCCACCAACCTTTGGCCAGGAGAGATACAGCAGGA 3286
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 538  GCAGAAATGATGGCTGAAACATATCATACATATGGGCAAGAAAGAAAGAAAGTGGAGTTG 597
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3287 TGGACTTACGGA 3298
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 598  GAGTCTAAAGGA 609
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-08-785-420-3
; Sequence 3, Application US/08785420
; Patent No. 6001976
; GENERAL INFORMATION:
; APPLICANT: MacLennan, David H
; APPLICANT: O'Brien, Peter J.
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
; TITLE OF INVENTION: HYPERTHERMIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte,
; STATE: No. 6001976th Carolina 28234
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

Query Match      1.1%; Score 53.6; DB 3; Length 1598;
Best Local Similarity 57.0%; Pred. No. 2.2e-05;
Matches 98; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 2066 GACCTAAAGTACTAGATGCTATGTTCACTCTGCGTACGCGTAAACGGGTGCGGTGCGC 2125
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 936  GACCCCTAGTGTGCTGATGCTCTGTTCCCTGTGTGTGTCATGTCATGTCGCGC 995
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2126 TCGTCACAGAACAACTCTGCGACTATTTGTCGTCGCCGCAAGAACCTGTTGCTGCAAACT 2185
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 996  TCCAACCAAGATCTCATTAAGAACTTGTCTCCGCGCGAGCTTCTGCTGCAGACA 1055
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2186 GCGCTTGTAGTACGATGCTATGTCGTCGTCGACACATCTTCGTGGGCGGAG 2237
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1056 AACCTCATCAACTATGTCAACGAGTGTGCGCCGCCCAACCTTTGACCCCGAG 1107
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
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Db 305 TTTCTGTAGATGCTGCCCATGTTATATAGTCCCGAGCCATTGACATGAGCAATGTTACAC 364  
Qy 3204 TGACACCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACCCACAACTTTGGG 3263  
Db 365 TATCAGAGACTGCTGATGCTATGGCAGAAATGATGGCTGAAAATATCATTAACATATGGG 424  
Qy 3264 CCAGGAGAGGATACAGCAGGAGTGGACTTACGGA 3298  
Db 425 CAAGAAAGAAACTGGAGTTGGAGTCTAAAGGA 459

## RESULT 9

US-09-668-097A-35  
; Sequence 35, Application US/09668097A  
; Patent No. 6673988

GENERAL INFORMATION:

; APPLICANT: Cahoon, Edgar B.

; APPLICANT: Cahoon, Rebecca E.

; APPLICANT: Klein, Ted

; APPLICANT: Shen, Jennie

; TITLE OF INVENTION: Plant Lipases

; FILE REFERENCE: B1401 US NA

; CURRENT APPLICATION NUMBER: US/09/668,097A

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/157309

; PRIOR FILING DATE: 1999-10-01

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 35

; LENGTH: 1334

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-668-097A-35

Query Match 0.8%; Score 40.8; DB 3; Length 1334;  
Best Local Similarity 58.1%; Pred. No. 0.21;  
Matches 72; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 1864 CAACACAGCACTGCGCGGATTCGCGAACTCGAACCGTTCAACTGGCTGTTCTCGCG 1923  
Db 728 CAACGCGCGACTACGACCACTAGCGTCTGAAGCGGTTCACGCGCTGTCGCGCCG 787  
Qy 1924 CTTGGCTCGAGGCTCGCGAGGCGCACCGGATGCTCGACGTGCTGCACTGCATCCT 1983  
Db 788 CCACAACTCGTCTCCAGAGCAGGTGACCACTGCGAGCAAGTACCCCTAGCCAA 847  
Qy 1984 CATC 1987  
Db 848 GATC 851

## RESULT 10

US-09-252-991A-11838

; Sequence 11838, Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 11838

; LENGTH: 294

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-11838

Query Match 0.8%; Score 39.4; DB 3; Length 294;  
Best Local Similarity 52.8%; Pred. No. 0.19;  
Matches 85; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 3280 GCAGGGATGACTTACGGACTTAATGAGGACTCGGACATGCATCGATCCCGCACCTGGT 3339  
Db 84 GCAGCAGCAGCCCTACGAGCCCAACCCGGAATCGAATCGCTCGCCAGCAGCTACGTGA 143  
Qy 3340 GCCATACCCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGAACACAGCTCGGAGAC 3399  
Db 144 AGGGCGCTGGACATCGCCCGGTGATCTACAAGACCGACTGTGGAGCGCTGTGGAT 203  
Qy 3400 TGTGAGGAGCCCTGCTGTGCTACGGGTATATGCTGGACCCGC 3440  
Db 204 CGTCCCGCGCGCTGCTTACGAGGACTCGCAGGGCGAGC 244

## RESULT 11

US-09-485-529-13

; Sequence 13, Application US/09485529

; Patent No. 6762348

GENERAL INFORMATION:

; APPLICANT: Harberd, Nicholas P

; APPLICANT: Richards, Donald E

; APPLICANT: Peng, Jinhong

; TITLE OF INVENTION: Genetic Control of Plant Growth and Development

; FILE REFERENCE: 620-91

; CURRENT APPLICATION NUMBER: US/09/485,529

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: PCT/GB98/02383

; PRIOR FILING DATE: 1998-08-07

; PRIOR APPLICATION NUMBER: GB 9717192.0

; PRIOR FILING DATE: 1997-08-13

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 1768

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-485-529-13

Query Match 0.8%; Score 38.6; DB 3; Length 1768;  
Best Local Similarity 47.6%; Pred. No. 1.2;  
Matches 147; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

Qy 1873 GAACCTGCGCGAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCTCGGCTC 1932  
Db 573 GAAGCTCGCCAGTTTCGCGCACACCATCCGCGTGCATTCAGTACCGCGCTCGTCCG 632  
Qy 1933 GCAGGCTCGGGCGAGGGCACCGGCATGCTCGAGCTGCTGCATCTCTCATCGACTC 1992  
Db 633 ---CGCCAGCTCGCGACCTGGAGCCGTTTCATGTCAGCGGAGGAGGAGGCC 689  
Qy 1993 GCCTGAAGCGCTCAATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2052  
Db 690 GAACGAGGAGCGCGAGGTAACTCGCGTCAACTCGCTCTTCGAGATGCAACCGGCTGC 749  
Qy 2053 AAAGCAGGAGCGGACCCCTAAAGTACTAGATGTTGTTCACTCTCGGTCGGTAAACGG 2112  
Db 750 GCAGCCCGGCGCCCTTGAGAGAGGTCCTGGGACCGTGGCGCCCGTGGCGCCAGGATCGT 809  
Qy 2113 CGTGGGCTGCGCTCGTGCACAGAAACATCTGGGACTATTTGCTGCGCGGCAAGAACT 2172  
Db 810 CACGCTGTTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 869  
Qy 2173 GTTGTGCA 2181  
Db 870 GTCTGTGCA 878

## RESULT 12

US-09-485-529-14

; Sequence 14, Application US/09485529



Patent No. 6762348  
; GENERAL INFORMATION:  
; APPLICANT: Harberd, Nicholas P  
; APPLICANT: Richards, Donald E  
; APPLICANT: Peng, Jinrong  
; TITLE OF INVENTION: Genetic Control of Plant Growth and Development  
; FILE REFERENCE: 620-91  
; CURRENT APPLICATION NUMBER: US/09/485,529  
; CURRENT FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: PCT/GB98/02383  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: GB 971192.0  
; PRIOR FILING DATE: 1997-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 2125  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-09-485-529-14

Query Match 0.8%; Score 38.6; DB 3; Length 2125;  
Best Local Similarity 47.6%; Pred. No. 1.4;  
Matches 147; Conservative 0; Mismatches 159; Indels 3; Gaps 1;  
  
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Db |||||  
Qy 1194 GAAGCTCGCCAGTTCGGCAACCATCCGGTCCGACTTCAGTACCGCGCCCTCGTCGC 1253  
Db |||||  
Qy 1933 GCAGGCTCGGGCGAGGCGACCGCATGCTCGAGCTGTGTGACATCTCTCATCGACTC 1992  
Db |||||  
Qy 1254 ---GCCACGCTCGGACCTGGAGCGCTTCATCTCGAGCGGCGGAGGAGACCC 1310  
Db |||||  
Qy 1993 GCCTGAAGCGCTCAATATGATGAGGAGCGAACAACATAAAGTGATATCTCTATTAGA 2052  
Db |||||  
Qy 1311 GAACGAGGAGCGCGAGGTAAATCGCGTCAACTAGTCTTCGAGATGCAACCGGCTGCTCGC 1370  
Db |||||  
Qy 2053 AAACGAGGAGCGGACCCCTAAAGTACTAGATGTGCTATGTTCACTCTCGCTCGTAACGG 2112  
Db |||||  
Qy 1371 GCAGCGCGCGCCCTGGAGAAAGTCTCTGGGACCGTGGCGCGCTGCGGCCCGAGATCGT 1430  
Db |||||  
Qy 2113 CGTCGGGTGGGCTCGTACAGAAACATCTGGAGTATTGCTGCCCGCGAAGAACCT 2172  
Db |||||  
Qy 1431 CACGCTGTGAGGAGGAGGCGGAATCAACTCCGGACATCTCTGGACCGCTTCACCGA 1490  
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Qy 2173 GTTCTGCA 2181  
Db |||||  
Qy 1491 GTCTGCA 1499  
Db |||||

RESULT 13  
US-09-502-540-5006  
; Sequence 5006, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/502,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5006  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-502-540-5006

Query Match 0.8%; Score 38.2; DB 3; Length 1290;

Best Local Similarity 56.4%; Pred. No. 1.3;  
Matches 92; Conservative 0; Mismatches 68; Indels 3; Gaps 1;  
  
Qy 1864 CAACACAGAACTGCGCGCAGTTCGGAACTCGAACCAGTTCGAATGGTGTTCGCG 1923  
Db |||||  
Qy 906 CAACAGAACTGAGCGCGTTCAGCGCAACGAGTACCGGGTGGGACCGTGTCTCGCCAG 965  
Db |||||  
Qy 1924 CTTGGCTCGCAGGCTTCGGGGGAGGCGACCGCATGCTCGAGTGTCTGCACTGCATCCT 1983  
Db |||||  
Qy 966 CGCGCTTACCAGGCC---GGCGAGGCCACCGTCAACGGAGTGTCTGTGGCGCAT 1022  
Db |||||  
Qy 1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGAGCGAACAC 2026  
Db |||||  
Qy 1023 CGTCGCTCGTACACGACGAGAGACGACGACGCCCGGCTC 1065  
Db |||||

RESULT 14  
US-09-902-540-1036  
; Sequence 1036, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1036  
; LENGTH: 12950  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(12950)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1036

Query Match 0.8%; Score 38.2; DB 3; Length 12950;  
Best Local Similarity 56.4%; Pred. No. 7.1;  
Matches 92; Conservative 0; Mismatches 68; Indels 3; Gaps 1;  
  
Qy 1864 CAACACAGAACTGCGCGCAGTTCGGAACTCGAACCAGTTCGAATGGTGTTCGCG 1923  
Db |||||  
Qy 1307 CAACAGAACTGAGCGCGTTCAGCGCAACGAGTACCGGGTGGGACCGTGTCTCGCCAG 1366  
Db |||||  
Qy 1924 CTTGGCTCGCAGGCTTCGGGGGAGGCGACCGCATGCTCGAGTGTCTGCACTGCATCCT 1983  
Db |||||  
Qy 1367 CGCGCTTACCAGGCC---GGCGAGGCCACCGTCAACGGAGTGTCTGTGGCGCAT 1423  
Db |||||  
Qy 1984 CATCGACTCGCCTGAAGCGCTCAATATGATGAGGAGCGAACAC 2026  
Db |||||  
Qy 1424 CGTCGCTCGTACACGACGAGAGACGACGACGCCCGGCTC 1466  
Db |||||

RESULT 15  
US-09-621-976-8976  
; Sequence 8976, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm



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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
16172.197 Million cell updates/sec

Title: US-10-668-767-1\_COPY\_1\_5000

Perfect score: 5000

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Searched: 18892170 seqs, 6143817638 residues

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Maximum Match 100%

Listing first 45 summaries

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- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
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- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4570.8	91.4	15429	US-10-668-767-143	Sequence 143, App
3	4501.6	90.0	15405	US-10-668-767-129	Sequence 129, App
4	4472.8	89.5	15387	US-10-668-767-127	Sequence 127, App
5	4288.8	85.8	15303	US-10-668-767-145	Sequence 145, App
6	2185.8	43.7	16363	US-10-668-767-9	Sequence 9, Appli
7	2158.2	43.2	15606	US-11-097-143-22562	Sequence 22562, A
8	2078.2	41.6	15413	US-10-668-767-7	Sequence 7, Appli
9	1846	36.9	15845	US-10-668-767-3	Sequence 3, Appli
10	1835.2	36.7	15315	US-10-668-767-5	Sequence 5, Appli
11	1455.8	29.1	24236	US-11-097-143-22561	Sequence 22561, A
12	840.8	16.8	4078	US-10-305-720-1154	Sequence 1154, Ap
13	840.8	16.8	14302	US-10-276-774-552	Sequence 552, App
14	840.8	16.8	15731	US-10-887-553A-490	Sequence 490, App
15	831.4	16.6	15359	US-10-276-774-500	Sequence 500, App
16	831.4	16.6	15359	US-10-887-553A-489	Sequence 489, App
17	831.4	16.6	15359	US-10-450-763-4960	Sequence 4960, Ap

Sequence 48, Appli  
Sequence 491, App  
Sequence 1500, Ap  
Sequence 12305, A  
Sequence 2337, A  
Sequence 5796, Ap  
Sequence 17, Appli  
Sequence 8, Appli  
Sequence 18, Appli  
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Sequence 2405, Ap  
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Sequence 169265,  
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Sequence 169265,

#### ALIGNMENTS

#### RESULT 1

US-10-668-767-1

; Sequence 1, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BBI533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 15679  
; TYPE: DNA  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (251)..(15676)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (5515)  
; OTHER INFORMATION: n = c or g  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (13000)  
; OTHER INFORMATION: n = a or t  
US-10-668-767-1

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Best Local Similarity 100.0%; Score 5000; DB 8; Length 15679;									
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	61	TTATGGGACG	TGTCATTATTCGGAATTTAGAAATCATTTAGTGTGTGTGAACGGTTAAAAATG	120					
Db	61	TTATGGGACG	TGTCATTATTCGGAATTTAGAAATCATTTAGTGTGTGTGAACGGTTAAAAATG	120					
Qy	121	TGTTAA	CAGTCGCGTCAGCGTTGATTCAGAAAAACGGATTTATTTGTGCGTTTGAACG	180					
Db	121	TGTTAA	CAGTCGCGTCAGCGTTGATTCAGAAAAACGGATTTATTTGTGCGTTTGAACG	180					
Qy	181	CATGTGTGATG	CAATTTTCAGTGTTTATGGCAACGTTGCAAGCACTGACAGCTCTACTG	240					
Db	181	CATGTGTGATG	CAATTTTCAGTGTTTATGGCAACGTTGCAAGCACTGACAGCTCTACTG	240					
Qy	241	AGAAATCCAA	GATGCGGAAGCAGAGGGGGAGCAAGCGAGCAAGATCATGTTTCAATCTTT	300					
Db	241	AGAAATCCAA	GATGCGGAAGCAGAGGGGGAGCAAGCGAGCAAGATCATGTTTCAATCTTT	300					
Qy	301	CGCTAC	CGGAACATATGTTGTGCATGTCTGTGCACAGCAGGAGAGGGTGTCCCTGGC	360					
Db	301	CGCTAC	CGGAACATATGTTGTGCATGTCTGTGCACAGCAGGAGAGGGTGTCCCTGGC	360					
Qy	361	TGCCGA	AGGTCCTGGCAACCGGCACCTGTTCTTGAGAAATTTGCCGACAAAGACATACC	420					
Db	361	TGCCGA	AGGTCCTGGCAACCGGCACCTGTTCTTGAGAAATTTGCCGACAAAGACATACC	420					
Qy	421	GCCTGATC	TGTGCGCAGTGTGTTTGTTCATCGAACAGCGCTTTTCAGTAAGAGCTTTACA	480					
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Qy	481	GGAGTTGG	TAAACAGCTCGGGATCTGAAACTGGGAAAGAAACATTAGGTAAAGTACCGG	540					
Db	481	GGAGTTGG	TAAACAGCTCGGGATCTGAAACTGGGAAAGAAACATTAGGTAAAGTACCGG	540					
Qy	541	TTCTGGTTAT	CGTACGTACTATACGGGAATGCTATTCTTTTGGGACATCTTTAACAGTGA	600					
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Qy	601	TATGTACT	CGSCCTGTCAACATCATCATCCAGGATAAGCTGGCCTTTGACGTGGG	660					
Db	601	TATGTACT	CGSCCTGTCTCAACATCATCATCCAGGATAAGCTGGCCTTTGACGTGGG	660					
Qy	661	TCTGCA	ACAGCACTCCCAAGSTGAAGCCTGTGTGTGACCCCTGCATCCTGCCAGCAAA	720					
Db	661	TCTGCA	ACAGCACTCCCAAGSTGAAGCCTGTGTGTGACCCCTGCATCCTGCCAGCAAA	720					
Qy	721	GAGATCCG	AGGGCGAGAAGTGCAGTCCGAGATGACTTGNATTTCTAGTCTCCGTGGCCAT	780					
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Qy	781	TGAGAGAT	ACTTTGCACACCAACGAAGAGAACGAAGTATCGATAGTGAACCGCTGTTCCA	840					
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Db	841	CGTGAC	GCACCTGGTCCGTACAGCCCTATGGTATATCGAGGATGAAGTATGTGGG	900					
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Qy 4681 TGCTCGAAGGCTTAACCTTCAGATCAAGTCTCAGCGGCCAATCAAAGATATACGGCAT 4740
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Qy 4981 GGTGACCAACCCAGTACCCT 5000
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## RESULT 2

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US-10-668-767-143
; Sequence 143, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B01533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 15429
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; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15429)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv3
US-10-668-767-143
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Query Match 91.4%; Score 4570.8; DB 8; Length 15429;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 4638; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
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Db |||||
Qy 1 ATGCGGAAGCAGAGGGGGAGCAAGCGAGCAGAGATGATGTTTCAATCTTCGCTACCGAA 60
Db |||||
Qy 311 GACATGCTGTGCATGTCGTGCACAGCGACAGGAGAGAGGCTGCTTGGCTGCCGAAGGT 370
Db |||||
Qy 61 GACATGCTGTGCTGTGTCGTCACAGCGACAGGAGAGAGGCTGCTTGGCTGCCGAAGGT 120
Db |||||
Qy 371 CTGCGCAACCGGCACTGCTTCTTGGAGAAATATTGCCGACAAGACAATACCGCTGTACTG 430
Db |||||
Qy 121 TTGCGCAACCGGCACTGCTTCTTGGAGAAATATTGCCGACAAGACAATACCGCTGTACTG 180
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Qy 431 TCGCAGTGTGTGTTGTCATCGAAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 490
Db |||||
Qy 181 TCGCAGTGTGTGTTGTCATCGAAACAGGCGCTTTCAGTAAGAGCTTTACAGGAGTTGGTA 240
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Qy 491 ACAGCTGCGGGAATCTGAACCTGGAAAGAAATCTTAGTAAAGTACCGGTCTTGGTTAT 550
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Qy 241 ACGCTGCGGCTTCTGAACCTGGAAAGAAATCTTAGTAAAGTACCGGTCTTGGTTAT 300
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Qy 551 CGTACGCTACTATACGCGCAATGCTATTTCTTTCGACATCTTAAACAGTGTATGTACCTG 610
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Qy 301 CGTACGCTACTATACGCGCAATGCTATTTCTTTCGACATCTTAAACAGTGTATGTACCTG 360
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Qy 611 GCTGCTGTCAACATCATCCAGGATTAAGCTGGCTTTGACGTTGGTCTGTCACACAG 670
Db |||||
Qy 361 GCTGCTGTGACATCATCCAGGATTAAGCTGGCTTTGACGTTGGTCTGTCACACAG 420
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Qy 671 CACTCCCAAGTCAAGCTGCTGTCGACCTCTGTCATCTGCCAGCAACAGAGATCCGAG 730
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Qy 731 GCGGAGAAGTGCAGTTCGAGATGATGATTTCTAGTCTCCGTTGGCCATGTGAGAGATAC 790
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Qy 791 TTGCACACAACGAAAGAGAAACGAAGTATCGATAGTGAACGGCTGTTCCAGTGAACGAC 850
Db |||||
Qy 541 TTGCACACAACGAAAGAGAAACGAAGTATCGATAGTGAACGGCTGTTCCAGTGAACGAC 600
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Qy 851 TGGTGGTACAGCCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 910
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Qy 601 TGGTGGTACAGCCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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Qy 1031 GCCCGTTCTATGGCGCTTGGAGTGGCTTAGAACCAAGTGGCGCGAGGTTTCATTAAAC 1090
Db |||||
Qy 781 GCCCGTTCTATGGCGCTTGGAGTGGCTTAGAACCAAGTGGCGCGAGGTTTCATTAAAC 840
Db |||||
Qy 1091 TGGTACCATCTATGAGGATTCGGCACATCACTACTTGGAGATATCTTGGAGTTAACGAC 1150
Db |||||
Qy 841 TGGTACCATCTATGAGGATTCGGCACATCACTACTTGGAGATATCTTGGAGTTAACGAC 900
Db |||||
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Qy 1211 CTGCGCCAGGAGAGGATGATCAGAAAGCAAGTGTGTAGAAAGCAAGGACTTGGAGGTGATA 1270  
Db 961 CTGCGTCAGGAGAGGAGTGTACAGAAACAAAGTGTGTAGAAAGCAAGGACTTGGAGGTGATA 1020  
Qy 1271 GCGCGCCCATCATCAAGTACGGTGACTTCCACCGTCAATGTGCGAGCATTCGGAGACTGGC 1330  
Db 1021 GCGCGCCCATCATCAAGTACGGTGACTTCCACCGTCAATGTGCGAGCATTCGGAGACTGGC 1080  
Qy 1331 TTGTGGCTGTCTTATAAGTCTTACGAAACGAGAGAAAGCGGTGGGTAAAGTAAAGAG 1390  
Db 1081 TTGTGGCTGTCTTATAAGTCTTACGAAACGAGAGAAAGCGGTGGGTAAAGTAAAGAG 1140  
Qy 1391 AAGCAAGCGATTTCTCCAGGAAAGGCAAGATGGACGATGCGCTCGACTTCCAGGTCA 1450  
Db 1141 AAGCAAGCGATTTCTCCAGGAAAGGCAAGATGGACGATGCGCTCGACTTCCAGGTCA 1200  
Qy 1451 CAGGAGGAAGAAATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCTGCTGTCTACTAAG 1510  
Db 1201 CAGGAGGAAGAAATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCTGCTGTCTACTAAG 1260  
Qy 1511 TTTATCAATGGCTGGGAACTCTTCAAGAGAACCGTCTGCTCATGATGTTCTTCCGCTCA 1570  
Db 1261 TTTATCAATGGCTGGGAACTCTTCAAGAGAACCGTCTGCTCATGATGTTCTTCCGCTCA 1320  
Qy 1571 GTGAACCTGGGCGAGATGATGTGTTCTTGAAGATCTCACAACACTCTTCCGACAGCCC 1630  
Db 1321 GTGAACCTGGGCGAGATGATGTGTTCTTGAAGATCTCACAACACTCTTCCGACAGCCC 1380  
Qy 1631 GATGAGGATATGGAAACAGAAAGAAAGCAAAATTCGCGCCCTCCGCAACCGTCAAG 1690  
Db 1381 GATGAGGATATGGAAACAGAAAGAAAGCAAAATTCGCGCCCTCCGCAACCGTCAAG 1440  
Qy 1691 GACCTGTTCCAGAGAGAGGATCTGAACCTGATCTCGAGCTATAGACAAAGATCAAC 1750  
Db 1441 GACCTGTTCCAGAGAGAGGATCTGAACCTGATCTCGAGCTATAGACAAAGATCAAC 1500  
Qy 1751 GTGTCAGCTCCAGGGGTTCTGGCTGATTCCTGGCGGGAGACGAATCTGGAACAGAGC 1810  
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Qy 1931 TCGCAGGCTCGGGCGAGGGCACCGGATGCTCGACGCTGCTGCACTGCACTCATCGAC 1990  
Db 1681 TCGCAGGCTCGGGCGAGGGCACTGGCATGCTCGAGCTGCTGCACTGGCTGCTCATCGAC 1740  
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Qy 2171 CTGTTGCTCAAACTCGCTTGTAGATCAAGTATCTAGTGTCCGTCGGAACATCTTCGTG 2230  
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Qy 2231 GCGCAGTAGAAGGGTCGGCAGTGTATCCGAAATGGTACTTTCGAGGTGATCTATGGAACAC 2290  
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Db 3001 CACAACTTTGGCGCAGGAGAGGATACAGCAGGATGAGCTTACGGAATTAATGAGGAC 3060  
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Qy 4151 TTACGTCTCTCACTGCTGTGCATCTGTCATTAACAGATTCATGACGAGGACGAGAAAGGCC 4210
Db 3901 TTACGTCTCTCACTGCTGTGCATCTGTCATTAACAGATTCATGACGAGGACGAGAAAGGCC 3960
Qy 4211 AGGCGTTGGGTAGAAATCAAGGACCGCCACCGATCTTAATGAAGGACGAGTTGAAGCT 4270
Db 3961 AGGCGTTGGGTAGAAATCAAGGACCGCCACCGATCTTAATGAAGGACGAGTTGAAGCT 4020
Qy 4271 CAGATGTCGCGCCATATTGACACAGATCATGAGGAGCGGTTTTCACCATGAACGATTTAAA 4330
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Qy 4331 GGTTTGGCACTACGAAGACAATCAGGAAGAGTTGCCAGCTCCAAGATGAAGCGCTGCT 4390
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Qy 4391 TCAAGGCCACACGTAAGGGATCCATGACAGAGGTGTTACTATACAAAATTACAATAAT 4450
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Db 4201 TTGCAACCGAGGCCAAGTCAATGGCATGCACCGGTGACCCAGTGAAGTGAATGGCCAAAG 4260
Qy 4511 TATGACTTGGGAGCGCAAGGTTTTCAGCGCTGATGATAAGAAAGCAAGAGGGGACGATCG 4570
Db 4261 TATGACTTGGGAGCGCAAGGTTTTCAGCGCTGATGATAAGAAAGCAAGAGGGGACGATCG 4320
Qy 4571 CCTTTCAAGTTCTTTTCAAGAACAAAGCGCGGCGAAAGCAGTGCATCGTGTAAATCCCGTAAA 4630
Db 4321 CCTTTCAAGTTCTTTTCAAGAACAAAGCGCGGCGGCGAAAGCAGTGCATCGTGTAAATCCCGTAAA 4380
Qy 4631 TCCAAACACACGACACCCCTTCAGTGATACCGAAGTATCACAGAACGTTGGTGTGCGAAGG 4690
Db 4381 TCCAAACACCTCCAGATCCCTTCAGCGATACCGAGGTATCACAGAACGTTGGTGTGCGAAGG 4440
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Qy 4871 ACTGTGGCAATCAGATCTTCGATGACAGGTGTTGAAGCTCATCAATGATGACTTTTAT 4930
Db 4621 ACTGTGGCAATCAGATCTTCGATGACAGGTGTTGAAGCTCATCAATGATGACTTTTAT 4680
Qy 4931 GGAGTCAGGATCTACCCAGGTCAAGACCCCAACCATGTCATCGCTGGGTGACCAAC 4990
Db 4681 GGAGTCAGGATCTACCCAGGTCAAGACCCCAACCATGTCATCGCTGGGTGACCAAC 4740
Qy 4991 CAGTACCACT 5000
Db 4741 CAGTACCACT 4750
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## RESULT 3

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US-10-668-767-129
; Sequence 129, Application US/10668767
; Publication No. US2004017114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: B01533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 15405
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15402)
; OTHER INFORMATION:
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FEATURE:  
OTHER INFORMATION: pXL-HV2  
US-10-668-767-129

Query Match 90.0%; Score 4501.6; DB 8; Length 15405;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 4614; Conservative 0; Mismatches 109; Indels 27; Gaps 2;

QY 251 ATGGCGGAAGCAGAGCGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTCGGTACGGAA 310  
DB 1 ATGGCGGAAGCAGAGCGGGGAGCAAGCGAGCAAGATGATGTTTCAATCTTCGGTACGGAA 60  
QY 311 GACATGTGTGTCATGTCGTCACAGCGACGAGAGAGGGTGTGCTGGCTGCCGAAGGT 370  
DB 61 GACATGTGTGTCATGTCGTCACAGCGACGAGAGAGGGTGTGCTGGCTGCCGAAGGT 120  
QY 371 CTCGGCAACCGGCACCTGCTTCTGAGAAATATTGCCGACAGAAATACCCGCTGATCTG 430  
DB 121 TTGGGCAACCGGCACCTGCTTCTGAGAAATATTGCCGACAGAAATACCCGCTGATCTG 180  
QY 431 TCGCAGTGTGTTTGTCTCATCGAACAGCGCTTTTCAGTAAGAGCTTTTACAGAGTTGGTA 490  
DB 181 TCGCAGTGTGTTTGTCTCATCGAACAGCGCTTTTCAGTAAGAGCTTTTACAGAGTTGGTA 240  
QY 491 ACAGCTCGGGATCTGAAACTGGGAAAGAAACTTAGGTAAAGGTACCGGTTCTGGTTAT 550  
DB 241 ACGGCTCGGGTCTGAACT-----GGTAAAGGTACCGGTTCTGGTCA 285  
QY 551 CGTACGCTATATACGGCAATGCTATCTTTTGGCAATCTTAAACAGTATATGATCTG 610  
DB 286 CGTACGCTATATACGGCAATGCTATCTTTTGGCAATCTTAAACAGTATATGATCTG 345  
QY 611 GCCTCGCTGTCACATCATCTCCAGATAGCTGGCTTTGAGCTGGCTGTCACAG 670  
DB 346 GCCTCGCTGTCACATCATCTCCAGATAGCTGGCTTTGAGCTGGCTGTCACAG 405  
QY 671 CACTCCCAAGGTGAAGCTGCTGGTGGACCTGTCATCTGCCAGCAAAACAGAGTCCGAG 730  
DB 406 CACTCCCAAGGTGAAGCTGCTGGTGGACCTGTCATCTGCCAGCAAAACAGAGTCCGAG 465  
QY 731 GCGGAGAGGTGCGAGTGGAGATGACTTGAATCTTCTGCTGGCCATTTGAGAGATAC 790  
DB 466 GGTGAGAGGTGCGAGTGGAGATGACTTGAATCTTCTGCTGGCTGCTGAGAGATAC 525  
QY 791 TTGCAACACGAAAGAGAAACGAAATATCGATAGTGAACGGCTGTTCCAGTGAAGCAC 850  
DB 526 TTGCAACACGAAAGAGAAACGAAATATCGATAGTGAACGGCTGTTCCAGTGAAGCAC 585  
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DB 586 TGGTCGGTACAGCCCTATGGTACTGGTATATCGAGATGAAGTATGTTGGCTATGTTTC 645  
QY 911 GGAGGTGATGCTCAGGTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGCACT 970  
DB 646 GGAGGTGATGCTCAGGTCTTCCATGGAGGTGACGAGTGTCTCACTATACCTAGTACC 705  
QY 971 TGGCAAAAGGATGGGGGCAAAATATCGTAGTCTCAAAAGGAGTTTCAATGATCTCAA 1030  
DB 706 TGGCAAAAGGATGGGGGCAAAATATCGTAGTCTCAAAAGGAGTTTCAATGATCTCAA 765  
QY 1031 GCCCGTTCTATGGCGCTGAGCTGGCTAGAACCAAGTGGCGGAGGTTTCAATTAAC 1090  
DB 766 GCCCGTTCTTATGGCGCTGAGCTGGCTAGAACCAAGTGGCGGAGGTTTCAATTAAC 825  
QY 1091 TGGTACCATCTATGAGGATTCGGACATCACTACTGGAAGATATCTCGAGTAAACGAC 1150  
DB 826 TGGTACCATCTATGAGGATTCGGACATCACTACTGGAAGATATCTCGAGTAAACGAC 885  
QY 1151 CAGAAATGAGCTGATTTAGTACGAGAGAAACCAACAGCTTCTGTCCTTCTGC 1210  
DB 886 CAGAAATGAGCTGATTTAGTACGAGAGAAACCAACAGCTTCTGTCCTTCTGC 945  
QY 1211 CTGGCCAGGAGAGATGATCAGAAAGCAAGTGTGTTAGAGCAAGGACTTGGAGTCA 1270

DB 946 CTGCGTCAGGAGAAAGGATGATCAGAAACAAAGTGTGTTAGAGCAAGGACTTGGAGTCA 1005  
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DB 1006 GGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCAATTGTGCAAGTATTCGAGACTGGC 1065  
QY 1331 TTGTGGCTGCTTTATAAGTCTTACGAAACGAGAAAGAGCGGTGGGTAAAGTGAAGAG 1390  
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DB 1126 AAGCAAGGATCTCCAGGAGGAGCAAGTGAAGTGGCTCGACTCTCCAGGTCA 1185  
QY 1451 CAGGAGCAAGAACTCTATGACTGCTCAGATTATCAGGAAGTGTCTTCTGCTGTTCAC 1510  
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DB 1246 TTTATCAATGGCTTGGAAACTCTTTCAAGAGAAACCGTCTGCTCACTCGATGTTCTTGC 1305  
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DB 1486 GTGCTACGCTCCAGGGGTTCTGCTGGATTCCTGGCGGAGAGCAATCTGGAAGAGC 1545  
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QY 1991 TCGCCTGAAGCGCTCAATATGATGAGGAGCAACACATATAAAGTGAATCTCTCTATTA 2050  
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QY 2051 GAAAGACGAGCGGACCGCTTAAAGTACTAGATGTGCTATGTTCACTCTGCGCTCGGTAA 2110  
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QY 2111 GCGCTGCGGCTGCGCTCGCTCAAGAAACATCTCGACTATTTGCTGCTGCGCGGCAAGAAC 2170  
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QY 2171 CTGTTGCTGCAAACTGCGCTTGTAGATCAAGTATCTAGTGTCCGTCGCAACTCTTCG 2230  
DB 1906 CTGTTGCTGCAAACTGCGCTTGTAGATCAAGTATCTAGTGTCCGTCGCAACTCTTCG 1965  
QY 2231 GGCGAGTAGAGGTCGCGAGTGTACCGCAATCTGCTAGTGTCCGTCGCAACTCTTCG 2290  
DB 1966 GGTCAGTAGAGGTCGCGAGTGTACCGCAATCTGCTAGTGTCCGTCGCAACTCTTCG 2025  
QY 2291 ATAGAGAGAGCACATATGATGCCACATCTAGCAGTAGGATGGCTTAACACTCTG 2350

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Qy 2351 TATGTCCCATACCGGGTGTGTGAGAGTGGGAGGTAAACGCGTGGGAGACGACCTG 2410  
Db 2086 TAGTCCCATACCGGGTGTGTGAGAGTGGGAGGTAAACGCGTGGGAGACGACCTG 2145  
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Qy 2471 AGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGTGTGTGATTTGGAC 2530  
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Qy 2531 CTGAGGTTACCCATCATCACTTCACTTCACTTCAACGGAGTGGGTTACGGGATCCTTCACC 2590  
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Qy 2711 CCGCTGTGTGAGTCTCTCTCCCGCAGAGATCCTCAGCTCTGGAGCGTCTTCTACTTC 2770  
Db 2446 CCGCTGTGTGAGTCTCTCTCCCGCAGAGATCCTCAGCTCTGGAGCGTCTTCTACTTC 2505  
Qy 2771 GGCAACCTGTCCAAAGCGGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT 2830  
Db 2506 GGCAACCTGTCCAAAGCGGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT 2565  
Qy 2831 GTGCTACGCGCTGTGTGATCTTTACAGATTACTCTGCTACATATGTGGAACAAATCAGA 2890  
Db 2566 GTGCTACACCTGTTGACACTTTACAGATTACTCTGCTACATATGTGGAACAAATCAGA 2625  
Qy 2891 GACAGCTAGCTGAAATATTCAGAAATGTGGGCTATGATAGATTCGAGCAGGCTGG 2950  
Db 2626 GACAAGCTAGCTGAAATATTCAGAAATGTGGGCTATGATAGATTCGAGCAGGCTGG 2685  
Qy 2951 ATGTACGGCGACAGAGAGAGCTTGACAAAGATCCACCCCTGCTCGTCCCTTCGAG 3010  
Db 2686 ATGTACGGCGATCAGAGAGAGACTTGACAAAGATCCACCCCTGCTCGTCCCTTCGAG 2745  
Qy 3011 CGACTCCCGCGCTGAGAAACGATACGATATACAACTTGTGTGACAGACTCAAGACT 3070  
Db 2746 CGTCTCCCGCGCTGAGAAACGATACGATATACAACTTGTGTGACAGACTCAAGACT 2805  
Qy 3071 ATCTGGGCTCTGGGCTACTACATCAGCTTAGATAGGCTCCAGCACGATCCGCAACGTT 3130  
Db 2806 ATCTGGGCTCTGGGCTACTACATCAGCTTAGATAGGCTCCAGCACGATCCGCAACGTT 2865  
Qy 3131 GGTCTGCCCAATGAACCTTTTCATCGAGTCCAAAGGCTACAGCCAGCACCTCGAGCTG 3190  
Db 2866 GGTCTGCCCAACGAACTTTTCATCGAGTCCAAAGGCTACAGCCAGCACCTCGAGCTG 2925  
Qy 3191 AGTCTGTCACTTCACCTGACACCCAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 3250  
Db 2926 AGTCTGTCACTTCACCTGACACCCAGATGGATGAGCTAGTAGGCCAGCTGGCTGAGAACACC 2985  
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Db 3166 CTGGACCCGCTACTCTGGGAGCAGCATGAAGCACTCTTGTGTGAAGCGTCAAAACAGAAAG 3225  
Qy 3491 CAAAGCGACTTTCAGAACATACCCGCGTGTGAGAGAACTATGCCCTCAGCTCTCGGAAAGTGG 3550  
Db 3226 CAAAGCGACTTTCAGAACATACCCGCGTGTGAGAGAACTATGCCCTCAGCTCTCGGAAAGTGG 3285  
Qy 3551 TACTTCGAGTTTGTAGATCCCTAAACGGCTGGACCTATGAGGCTCGCTGGGCTCAACGCTGAT 3610  
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Qy 3611 ATGGCACCCAGGAATGATGCTCGGACAAAGACGAGAACTCTCTGGGCTTTTGTATGTTTACAAT 3670  
Db 3346 ATGGCACCCAGGAATGATGCTCGGACAAAGACGAGAACTCTCTGGGCACTTTGTATGTTTACAAT 3405  
Qy 3671 GAGGAAAAAGTGTACAGCGGTAAACACTGAGTCTTTTCGGCAAGCAATGGGCTGTGTGTGAC 3730  
Db 3406 GAGGAAAAAGTGTACAGCGGTAAACACTGAGTCTTTTCGGCAAGCAATGGGCTGTGTGTGAC 3465  
Qy 3731 GTAGTGGGGTGTTCCTAGATCTCATTGATAAGACGATAAAGTTTCTCACTCAACGGTGAG 3790  
Db 3466 GTAGTGGGGTGTTCCTAGATCTCATTGATAAGACGATAAAGTTTCTCACTCAACGGTGAG 3525  
Qy 3791 TTCTTGTATGGATGCTCTTGGCGGAGAGACTACGTTTGTCTGATGTCCAGGGTGACAACTTT 3850  
Db 3526 TTATTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGTCTGATGTCCAGGGTGACAACTTT 3585  
Qy 3851 GTACTGCTTGTGACGCTTGGTGTTCGCGCAAAAAAGCAGGTTAAACATACCGTCAAGGAGTG 3910  
Db 3586 GTACTGCTTGTGACGCTTGGTGTTCGCGCAAAAAAGCAGGTTAAACATACCGTCAAGGAGTG 3645  
Qy 3911 AACACGCTGAAATACTTCAACATCTGTGTCTCGAGGAGGATATGAACCATCTGTGTGTC 3970  
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Qy 3971 AATATGAAGAGAGACGCTGACTCACTGGTACACCAAAGACAGCGCGATCTTCGAGAAATACG 4030  
Db 3706 AATATGAAGAGAGACGCTGACTCACTGGTACACCAAAGACAGCGCGATCTTCGAGAAATACG 3765  
Qy 4031 GATGAGATGATTCGACACCAAGATAGATGTGACCAAGATACCACTGGTTTCAGATACACCT 4090  
Db 3766 GATGAGATGATTCGACACCAAGATAGATGTGACCAAGATACCACTGGTTTCAGATACACCT 3825  
Qy 4091 CCATGGCTCAAGATTTTCCCAACACGTTTGTGACAGATGAGAGAAAGCTAACTGGAGTTC 4150  
Db 3826 CCATGGCTCAAGATTTTCCCAACACGTTTGTGACAGATGAGAGAAAGCTAACTGGAGTTC 3885  
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Db 3886 TTACGCTCTCTCACTGCTGCTATCTGCCATAACGAGTTTCAATTGACAGGCGAGAAAAAGCC 3945  
Qy 4211 AGCGTTTGGGTAGAAATCAAGGACCCGCAACCGGATCTTAATGAAAGAGGAGTTGAAAGCT 4270  
Db 3946 AGCGTTTGGGTAGAAATCAAGGACCCGCAACAGATCTTAATGAAAGAGGAGTTGAAAGCT 4005  
Qy 4271 CAGATGTCCGCCCATATTGACCCAGATCATGAGGCGGTTTCCACATGAACGATATTAAA 4330  
Db 4006 CAGATGTCCGCCCATATTGACCCAGATCATGAGGCGGTTTCCACATGAACGATATTAAA 4065  
Qy 4331 GGTTTGCACTTACGAAGCAATCAGGAAGAGTTGTCGCCAGCTCCCAAGATGAAGCGCTGCCT 4390  
Db 4066 GGTTTGCACTTACGAAGCAATCAGGAAGAGTTGTCGCCAGCTCCCAAGATGAAGCGCTGCCT 4125  
Qy 4391 TCAAGGCCACCAAGTAAAGGATCCATGAAGAGGTTGTTACTATACAAATTTACAATAAT 4450  
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Qy 4451 TTGCAACAGGCGCAAGTCAACGGCATGCAACGGTTCGACCGCTGAGGAGTGAAGTGGCCAAAG 4510  
Db 4186 TTGCAACAGGCGCAAGTCAATGGCATGCAACGGTTCGACCGCTGAGGAGTGAAGTGGCCAAAG 4245



QY 4511 TATGACTTGGAGCCGCAAGTTTGTGACGCTGATGATTAAGAGGACAAAGAGGGGACGATCG 4570  
DB 4246 TATGACTTGGAGCCGCAAGTTTGTGACGCTGATGATTAAGAGGACAAAGAGGGGACGATCG 4305  
QY 4571 CTTTTCAGTTCTTCAGAGCAAGCGCGGCAAGACGATGATCGTCTAATCCGTAATA 4630  
DB 4306 CTTTTCAGTTCTTCAGAGCAAGCGCGGCAAGACGATGATCGTCTAATCCGTAATA 4365  
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DB 4366 TCCAAAACTCCAGATCCCTTCAGCGATACCGAGGTATCACCAAGAACGCTGGTGCTCGAAGG 4425  
QY 4691 CTTAAACCTCAGATCAAGTGTACAGGCCAATCAAGATATAACCGCATGAACCGGT 4750  
DB 4426 CTTAAACCTCAGATCAAGTGTACAGGCCAATCAAGATATAACCGCATGAACCGGT 4485  
QY 4751 CTTACAGGACCAACTGTATGGGAGCCAGTTGGTTGAACTCGAACGCTCAGATGGCG 4810  
DB 4486 CTTACAGGACCAACTGTATGGGAGCCAGTTGGTTGAACTCGAACGCTCAGATGGCG 4533  
QY 4811 ACGCCACGCAAGACAGGAAGCAGATGACGACGACACTCTCGCGCAGTGGCTACGGAA 4870  
DB 4534 ACGCCACGCAAGACAGGAAGCAGATGACGACGACACTCTCGCGCAGTGGCTACGGAA 4593  
QY 4871 ACTGTGGCAATGAGATCTTCGATGCGAGAGTGTGTTGAAGCTCATCAATGAGTACTTTTAT 4930  
DB 4594 ACTGTGGCAATGAGATCTTCGATGCGAGAGTGTGTTGAAGCTCATCAATGAGTACTTTTAT 4653  
QY 4931 GGAGTCAGATCTACCCAGGTCAAGACCCCAACCCCATGATCATCGGCTGGGTGACAC 4990  
DB 4654 GGAGTCAGATCTACCCAGGTCAAGACCCCAACCCCATGATCATCGGCTGGGTGACAC 4713  
QY 4991 CAGTACCCT 5000  
DB 4714 CAGTACCCT 4723

RESULT 4

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; Sequence 127, Application US/10668767  
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; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B01533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
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; PRIOR APPLICATION NUMBER: 60/412,795  
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; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 127  
; LENGTH: 15387  
; TYPE: DNA  
; ORGANISM: Heliothis virescens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(15384)  
; OTHER INFORMATION:  
; FEATURE:  
; OTHER INFORMATION: pXL-Hv7  
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Query Match 89.5%; Score 4472.8; DB 8; Length 15387;  
Best Local Similarity 96.8%; Pred. No. 0;

Matches 4596; Conservative 0; Mismatches 127; Indels 27; Gaps 2;  
QY 251 ATGCGGAAGCAGAGGGGGGAGCAAGCAGCAAGATGATGTTTCAATCTTCGCGTACGAA 310  
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QY 311 GACATGTGTGCATGTGTGCACAGCGACAGAGAGAGGGGTGTGCTGGCTGCCGAAGGT 370  
DB 61 GACATGTGTGTGCTGTGTGCACAGCGACAGAGAGAGGGGTGTGCTGGCTGCCGAAGGT 120  
QY 371 CTGCGCAACCGGCACTGCTTCTCGAGAATATTCGCCACAAGAAACATACCCCTGATCTG 430  
DB 121 TTGCGCAACCGGCACTGCTTCTCGAGAATATTCGCCACAAGAAACATACCCCTGATCTG 180  
QY 431 TCGCAGTGTGTGTGTGTGCATCGAACAGCGCTTTTCAGTAAAGAGCTTTTACAGAGTGTGTA 490  
DB 181 TCGCAGTGTGTGTGTGTGCATCGAACAGCGCTTTTCAGTAAAGAGCTTTTACAGAGTGTGTA 240  
QY 491 ACAGTGTGGGATCTGAAACTGGGAAAGAAACTTAAAGGTACCGGTTCTGGTTAT 550  
DB 241 ACAGTGTGGGCTCTGAAACT-----GGTAAAGGTACCGGTTCTGGTTAT 285  
QY 551 CGTACGCTACTATACGGCAATGCTATTCTTTTGGACATCTTAAACAGTATGATGACCTG 610  
DB 286 CGTACGCTACTATACGGCAATGCTATTCTTTTGGACATCTTAAACAGTATGATGACCTG 345  
QY 611 GCCTGCCTGTCAACATCATATCCAGGATAGCTGGCTTTTGACGTGGGTCTGCAACAG 670  
DB 346 GCCTGCCTGTCAACATCATATCCCGGATAGCTGGCTTTTGACGTGGGTCTGCAACAG 405  
QY 671 CACTCCCAAGGTGAAGCCTGTGTGGACCTGTGATCTCTGCGACAAACAGAGATCCGAG 730  
DB 406 CACTCCCAAGGTGAAGCCTGTGTGGACCTGTGATCTCTGCGACAAACAGAGATCCGAG 465  
QY 731 GCGGAGAGGTGCGAGTGGAGATGACTTGAATCTAGTCTCCGTGGCCATGAGAGATAC 790  
DB 466 GGTGAGAGGTGCGAGTGGAGATGACTTGAATCTAGTCTCCGTGGCTACTGAGAGATAC 525  
QY 791 TTGCACACCAAGAGAGAAAGATATCGATAGTGAACGGCTCGTTCCACGTGACGAC 850  
DB 526 TTGCACACCAAGAGAGAAAGATATCGATAGTGAACGGCTCGTTCCACGTGACGAC 585  
QY 851 TGGTGGTACAGCCCTATGGTATATCGAGGATGAAGTATGTGGGTATGTGTTTC 910  
DB 586 TGGTGGTACAGCCCTATGGTATATCGAGGATGAAGTATGTAGGCTATGTATTC 645  
QY 911 GGAGTGTATGTCTCAGGTTCTTCCATGGAGGTGACGAGTGTCTCAGTATACCTAGCACT 970  
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QY 1031 GCCCGTTCTCTATGGCGCTGGAGCTGGCTAGAACCAAGTGGCGCGGAGTTTCAATTAAC 1090  
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QY 1091 TGGTACCAATCTATGAGGATTCGGGACATCATCTACTGGAAGATATCTGGAGTTAACGAC 1150  
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DB 946 CTGCGTACAGAGAGGATGATCAGAAAGCAAGTGTGTAGAGAACAGGACTTGGAGTCTATA 1005  
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QY	1331	TTGTGGCTGTCTTATAGTCTTACGAAACGAAAGAAAGCGCTGGGTAAAGTAGAAG	1390
Db	1066	TTGTGGCTGTCTTATAGTCTTACGAAACGAAAGAAAGGAGTGGGTAAAGTAGAAG	1125
QY	1391	AAGCAACGCGATTCTCCACGAGGAAGCAAGATGACGATGGCCCTCCAGCTCTCCAGGTCA	1450
Db	1126	AAGCAACGCGATTCTCCACGAGGAAGCAAGATGACGATGGCCCTCCAGCTCTCCAGGTCA	1185
QY	1451	CAGGAGAAAGATCTATGACTGTCTGAGTTATACAGGAAGTGTCTTTCGCTGTTCATTAAG	1510
Db	1186	CAGGAGAAAGATCTAGGACTGTCTGAGTTATCAGGAAGTGTCTTTCGCTGTTCATTAAG	1245
QY	1511	TTTATCAATGGCTGGGAAACTCTTCAGAGAACCGTGTCTCACTCGATGTTCTTCGGGTCA	1570
Db	1246	TTTATCAATGGCTGGGAAACTCTTCAGAGAACCGTGTCTCACTCGATGTTCTTCGGGTCA	1305
QY	1571	GTGAACCTGGCGAGATGGTGTCTTGAAGATCTCAACCAACTACTTTCGACACAGCCC	1630
Db	1306	GTGAACCTGGCGAGATGGTGTCTTGAAGATCTCAACCAACTACTTTCGACACAGCCC	1365
QY	1631	GATGAGGATATGGAACACGAAGAAAGCAAAATTCGCGCGCTCCGCAACCGGTCTAG	1690
Db	1366	GATGAGGATATGGAACACGAAGAAAGCAAAATTCGCGCGCTCCGCAACCGGTCTAG	1425
QY	1691	GACCTGTTCAGAGGAAGGCATCTGAACTGTATCTCGAGTCTATAGCAAGATCAAC	1750
Db	1426	GACCTGTTCAGAGGAAGGCATCTGAACTGTATCTCGAGTCTATAGCAAGATCAAC	1485
QY	1751	GTGCTCAGTCCAGGCGGTTCCTGGCTGGATTCTCGCGGAGACGAATCTGACACAGAC	1810
Db	1486	GTGCTCAGTCCAGGCGGTTCCTGGCTGGATTCTCGCGGAGACGAATCTGACACAGAC	1545
QY	1811	TGGGAAATGATATCTGGATTTTGATCAGTTGCTGGCGCAATPAATAAAGGCAACAC	1870
Db	1546	TGGGAAATGATATCTGGATTTTGATCAGTTGCTGGCGCAATPAATAAAGGCAACAC	1605
QY	1871	ACGAACTCGCGGAGTTTCGGAACTCGAACCGGTTTCAACTGGCTGTTCTCGCGCTCGGC	1930
Db	1606	ACGAACTCGCGGAGTTTCGGAACTCGAACCGGCTCAACTGGCTGTTCTCGCGCTCGGC	1665
QY	1931	TCGACAGCTCGGCGAGGCGACCGGATGCTCGACGTGTGCACTGCATCTCATCGAC	1990
Db	1666	TCGACAGCTCGGCGAGGCGACCGGATGCTCGACGTGTGCACTGCCTGCTTTATAGAC	1725
QY	1991	TCGCTTGAAGCGCTCAATATGATGAGGACGAAACACATAAAAGTGAATACTCTCTATTA	2050
Db	1726	TCGCTTGAAGCTCTCAATATGATGAGGACGAAACACATAAAAGTGAATACTCTCTATTA	1785
QY	2051	GAAAGCACGGAACGGACCTTAAAGTACTAGATGTGTATGTTTCACTCTGGTGGTAAAC	2110
Db	1786	GAAAGCACGGAACGGACCTTAAAGTACTAGATGTGTATGTTTCACTCTGGTGGTAAAC	1845
QY	2111	GGCGTCGGGTGCGCTCGTACAGAAACAACTATGCGACTATTGTCGCCGCGCAAGAAC	2170
Db	1846	GGCGTCGGGTGCGCTCGTACAGAAACAACTATGCGACTATTGTCGCCGCGCAAGAAC	1905
QY	2171	CTGTTGTGCAAACTGGCGCTGTGATCAGGTATCTAGTGTCCGTCCGAAACATCTTCGTG	2230
Db	1906	CTGTTGTGCAAACTGGCGCTGTGATCAGGTATCTAGTGTCCGTCCGAAACATCTTCGTG	1965
QY	2231	GGCGAGTAGAAGGGTCGGAGTGTACCGGAAATGGTACTCTTCGAGGTGACTATGGACAC	2290
Db	1966	GGTCCAGTAGAAGGGTCGGAGTGTACCGGAAATGGTACTCTTCGAGGTGACTATGGACAC	2025
QY	2291	ATAGAGAAGACCAACATATGATGCGCATCTACGATAGGTGGGTAAACACTTACTGTT	2350
Db	2026	ATAGAGAAGACCAACATATGATGCGCATCTACGATAGGTGGGTAAACACTTACTGTT	2085
QY	2351	TATGTCACATCCCGGGTGTGGTGTGAGAAGTGGGAGGTAAACCGCGTGGGAGACGACTG	2410
Db	2086	TATGTCACATCCCGGGGTTGGCGAGAAATGGGGAGGTAAACCGCGTGGGAGTGAACCTG	2145

QY	2411	TACTCGTACGGGTTTGATGGCGCTTACCTCTGGTCCGGGGAGGAAGACCCCGGTCAAT	2470
Db	2146	TACTCGTACGGGTTTCAACGGGCTTACCTCTGGTCCGGGGAGGAAGACTCCCGTCAAT	2205
QY	2471	AGGACTCATGTCTGAAGAGCTTATATTAGAAAGGTGAAGTATAGGTGTGTGATTGGAC	2530
Db	2206	AGGACTCATGTCTGAAGAGCTTATATTAGAAAGGTGAAGTATAGGTGTGTGCGATTGGAC	2265
QY	2531	CTGACGGTACCCATCATCACTTCACTGTTCAACGGAGTGGGTGACGGGATCCTTCACC	2590
Db	2266	CTGACGGTACCCATTAATCAACTTTCATGTTCAACGGAGTGGGTGACGGGATCCTTCACC	2325
QY	2591	AACCTTCAATCTGGAAGGCTATGTTCTTCCCGGTTCATCAGCTGTCTCTAGTAACTGAGTTGT	2650
Db	2326	AACCTTCAATCTGGAAGGCTATGTTCTTCCCGGTTCATCAGCTGTCTCTAGTAACTGAGTTGT	2385
QY	2651	CGGTTCTCTGCTGGGCGGAGAACCGGTAGACTCCGGTACGCGGCTCCAGAAAGGTACTCC	2710
Db	2386	CGGTTCTCTGCTGGGCGGAGAACACCGGTCTCTCCGGTACGCGGCTCCAGAAAGGTACTCT	2445
QY	2711	CGGTTCTGCTGGAGTCTCTCTGCGGACGAGATCCTCAGCTGGAGCGGCTCTTACTCTC	2770
Db	2446	CGGTTCTGCTGGAGTCTCTCTGCGGACGAGATCCTCAGCTGGAGCGGCTCTTACTCTC	2505
QY	2771	GGCAACCTGTCCAAAGCGGCGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTT	2830
Db	2506	GGCAACCTGTCCAAAGCGGCGCTTGGCTGGACCTCCGCTAGTACAGGACGATACGGCTTT	2565
QY	2831	GTGCTTACCGCTGTGTGATATTTACAGATTATCTCTGCTTACATATGTGGAAACAAATCAG	2890
Db	2566	GTGCTTACACCTGTGTGATATTTACAGATTATCTCTGCTTACATATGTGGAAACAAATCAG	2625
QY	2891	GACAACTAGCTGAAATATTTACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG	2950
Db	2626	GATAAGCTAGCTGAAATATATACGAAATGTGGGCTATGAATAAGATCGAAGCAGGCTGG	2685
QY	2951	ATGTACGGCGACCCAGAGAGAACTTGGCAAGATCCACCCCTGCTCTGCGCTTCGAG	3010
Db	2686	ATGTACGGCGACCCAGAGAGAACTTGGCAAGATCCACCCCTGCTCTGCGCTTCGAG	2745
QY	3011	CGACTCCCGCGCTCGAGAAACGATACGATATAAATTCTGCTGTGAGACACTCAAGACT	3070
Db	2746	CGACTCCCACTCTGCTGAGAAACGATACGATATAAATTCTGCTGTGAGACACTCAAGACT	2805
QY	3071	ATCTTGGCTCTGGGCTACTACATCAGCTTAGATAAGCTCCAGCAGCATCCGCAACGTT	3130
Db	2806	ATCTTGGCTCTGGGCTACTACATCAGCTTAGATAAGCTCCAGCAGCATCCGCAACGTT	2865
QY	3131	CGTCTCCCAATGAACTTTTTCATGCAAGTCCAAAGGCTTCAAGCCAGCACCACCTG	3190
Db	2866	CGTCTCCCAATGAACTTTTTCATGCAAGTCCAAAGGCTTCAAGCCAGCACCACCTG	2925
QY	3191	AGTGTGTCTCACTCTGACACCCAAAGATGGATAGCTAGTAGGCGAGCTGGGTGAGAACACC	3250
Db	2926	AGTGTGTCTCACTCTGACACCCAAAGATGGATAGCTAGTAGGCGAGCTGGGTGAGAACACC	2985
QY	3251	CACAACTTTGGGCGGAGGAGATACAGCAGGATGGACTTACGAGCTTATATGAGGAC	3310
Db	2986	CACAACTTTGGGCGGAGGAGATACAGCAGGATGGACTTATGAGCTTATATGAGGAC	3045
QY	3311	TCGGACATGATCGATCCCGCACCTTGGTGCATACCCGAAAGGTTCAGATGCCATCAAG	3370
Db	3046	TCGGACATGATCGATCCCGCACCTTGGTGCATACCCGAAAGGTTCAGATGCCATCAAG	3105
QY	3371	AAGGCCAAACAGGAGACAGCTTCGGAGACTGTGAGGACCTGTGTGTTTACGGGTATATG	3430
Db	3106	AAGGCCAAACAGGAGACAGCTTCGGAGACTGTGAGGACCTGTGTGTTTACGGGTATATG	3165
QY	3431	CTGGACCCCGCTTACTGGGAGCAGCATGAAGCACTCTTGTGGAAGCGTCAAAACAAAG	3490
Db	3166	CTGGACCCCGCTTACTGGGAGCAGCATGAAGCACTCTTGTGGAAGCGTCAAAACAAAG	3225
QY	3491	CAAGCCGACTTTCAGAAACATACCGCGCTGAGAAACATATGCCGTCTAGCTCTGGGAGTGG	3550







Qy 4691 CCTAACCTCAGATCAAGTGTACAGCCCAATCAAGATATATACGCATGAACGCGGT 4750  
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Qy 4751 CCTAGCAGGACCAACCTGTATGGGAGCCAAAGTTGGTTTGAACCTCGAACGCTCAGATGGCG 4810  
Db |||||  
Qy 4811 ACGCCACGCAAGACAGAGACAGATGACACACGACATCTCGGCGAGTGGGTACGGAA 4870  
Db |||||  
Qy 4871 ACTGTCGCAATGAGATCTTCGATGACAGAGTGTGAGGCTCATCAATGAGTACTTTAT 4930  
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Qy 4931 GGAGTCAGGATCTACCCAGGTCAAGACCCCAACCATGATACATCGGCTGGGTGACCAAC 4990  
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Qy 4630 CAGTACCCT 4639

## RESULT 6

US-10-668-767-9  
; Sequence 9, Application US/10668767  
; Publication No. US2004017114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B01533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 16363  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15890)..(15890)  
; OTHER INFORMATION: n = a, c, g, or t  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(15327)  
; OTHER INFORMATION:  
US-10-668-767-9

Query Match 43.7%; Score 2185.8; DB 8; Length 16363;  
Best Local Similarity 70.7%; Pred. No. 0;  
Matches 2983; Conservative 0; Mismatches 1192; Indels 42; Gaps 4;

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Qy 63 GGTACAGCTCTCTCGTGCACGGGACGGGGAGCGGTCTGCTTGGCCCGCGAAGGATTGG 122

Qy 376 CAACCGGCTGCTTCTCGAGAAATATTGCCGAAGAACAATACCGCTGATCTGTGCA 435  
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Qy 436 GTGTGTTTGTTCATCGAACAGCGCTTTTACGTAAGAGCTTTTACAGAGTTGTGTAAACAG 495  
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Qy 496 TGGGGATCTGAACCTGGGNAAGAAACCTTAGTAAAGGTACCGTCTTGTGTTATCGTAC 555  
Db |||||  
Qy 556 GCTACTATACGGCAATGCTATTCTTTTGGACATCTTAAACAGTATATGTAACCTGGCCTG 615  
Db |||||  
Qy 616 CTGTCAACATCATATCCAGGATTAAGCTGGCTTTTGAAGCTGGGTCTGCAACAGCACTC 675  
Db |||||  
Qy 676 CCAAGGTGAACCTGCTGGTGGACCTGTGATCTGCGCAGCAACAGAGATCCGAGGGCGA 735  
Db |||||  
Qy 736 GAAGGTGCGAGTCGGAGATGACTTGTATCTTAGTCTCGTGGCCATTGAGAGATCTTGCA 795  
Db |||||  
Qy 796 CACAACGAAGAGAACAAAGTATCGATAGTGAACGCGTCTTCCAGTGAACGACTGGTC 855  
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Qy 1456 GGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCGCTGTTTCACTAAGTTTAT 1515



Db	1188	CGAGGAGTCCAAGACGGCTCGTGTATCCGCAAGTGCAGCAGCTCTTCAACCCAGTTTAT	1247	Db	2268	TGTGCCCATCATACAGTTTACTTTTAAACGGAGTAAAGTGCAGCGGTAGCTTTTAGGACTT	2327
Qy	1516	CAATGGCCTGGAACTCTCTTAAGAGAACCGTGGTCACTCGATGTCTTTCGGCTCAGTGA	1575	Qy	2596	CAATCTGAAAGGCATGTCTTCCCGGTCAATCAGCTGTCTTAGTAAGCTGAGTTGTCGGTT	2655
Db	1248	TACAGCCTTGGAAACACGTGACGTCAAAATCGCCGACACTCCATTTTCTTCAAAAAGGTCAA	1307	Db	2328	TAACTTGACCGAATGTCTTCCCGTGAAGTTGCTCATCAAAACTAAAGCTGTCGCTT	2387
Qy	1576	CTGGGCGAGATGGTGATGTCTTGAAGATCTCACCAACTACTTTCGCACAGCCGATGA	1635	Qy	2656	CCTGTGGCGGAGAACAGGTAGACTCCGGTACGCGGTCCAGAAAGGTACTCCCCCGT	2715
Db	1308	CCTCAACGAGATGGTCACTGTGCTTGAGGACTTGATTAACACTTTTCGCAACCGAAGA	1367	Db	2388	CTTTTTCGAGGTGATCATGTGTCTTAAAGTTTCCCGCCGCTTGGGATTTCTCTGCGCT	2447
Qy	1636	GGATATGGAACACGAAGAAACAAACAAATTCGCGCCCTTCGCAACCGTCAGACCT	1695	Qy	2716	GGTGGAGTCTCTCTGCGCGACGACATCTCAGCTCGAGCGGTCTTCTACTCTCGGCAA	2775
Db	1368	CGATATGGAGCACGAGGAAACAGAACCGATTTCGTCGCCCTCGCAACCGACAGATCT	1427	Db	2448	CGTCAGTGTCTCATGCGCGACAGATCTCAGTCTGGATCTTCTCTTCTACTTTGGTAA	2507
Qy	1696	GTTCCAAGAGGAAGCATACTGAACTCTGATCTCTGAGCTATAGACAGATCAACGTGT	1755	Qy	2776	CCTGTCCAAAGCGGGCTTGGCTGGACCCCGCTAGTACAGGACGATACGGCTTTTGTGCC	2835
Db	1428	GTTCAGGAGGAGGGCTGCTCAATCTGATCTCTGGAGGCCATGCAAGGTCAACATAAT	1487	Db	2508	TCCTGCCAAGAAATGTTTTGGCGGACCATGCTTATTGAGGACGACACTGCTTTTGTTC	2567
Qy	1756	CACGTCCACAGGGTTCCTGGCTGGATTCTCTGGCGGAGACGAATCTGGACAGAGCTGGGA	1815	Qy	2836	TACGCTCTTGTATCTTTACAGATTAATCTCTGCTTACATATGTGGAACAAATCAGAGACAA	2895
Db	1488	CACCTCGCAGGGCTTCTAGCAGCTTCTTGCGCGGACGAGACCGGCCAGAGCTGGGA	1547	Db	2568	GAAAGCCGTGTATACCAAGGGTGTGACATTTGCCAAGTTCTGTGGACCAAAATCAAGAGAA	2627
Qy	1816	AATGATATCTGGATATTTGTATCAGTTGCTGGGCAATTAATAAAGGCAACCAACGAA	1875	Qy	2896	GCTAGCTGAAATATTACGAAATGTGGCTATGAATAAGATCGAAGCAGGCTGGATGTA	2955
Db	1548	TCTCATCTCCACTATTGTACCAACTCTTGGCGCCATCATCAAGGGCAACACACGAA	1607	Db	2628	GCTGCGGAGAAATATCCACGAGATGTGGGCTCTAAACAAATTCGAAGCGGCTGTGCTG	2687
Qy	1876	CTGGCGGAGTTCGGAACCTCGAAACCGGTTCAACTGGCTGTCTCGCGCTCGGCTCGCA	1935	Qy	2956	CGGACACAGAGAGAGAACTTGCACAAATCCACCCCTGCCTCTGCTGCCCTTCGAGCGACT	3015
Db	1608	CTGCGCCCACTTCGCGAAACAGTAACCGACTCAACTGGCTATTCTCCCGCTCGGTTCCCA	1667	Db	2688	GGCGAGCACCGAGATGACTACCAACCGCATTCATCTTCTGCTCACCCTTTTCGAGAGCT	2747
Qy	1936	GGCTCGGCGAGGGCACCGGATGCTCGACGTGCTGCACTGCATCTCATGACTCGGC	1995	Qy	3016	CCGCGCCCTGAGAAACGATACGATATACAACTTCTGTGCGACACACTCAAGACTATCT	3075
Db	1668	GGCTTCAGCGAGGGTTCGGCAATGTTGACGTACTTCACTGGCTGATCGATTGCGC	1727	Db	2748	TCGCGCGGGAAGACGATACGACAAATCACTAGCTGTGCAAAACGCTGAAGACGATTAT	2807
Qy	1996	TGAAGCGCTCAATATATGATGAGGAGCAACACATAAAGTGAATAATCTCTATTAGAAA	2055	Qy	3076	GGCTCTGGGCTACTACATCAGCTTAGATAAGCTTCAGACGCAATCCGCAAGCTTCGTC	3135
Db	1728	AGAGGACTTAACATGATCGGGATGAGCACATCAAGTGGTCACTCCCTCTCGAGAA	1787	Db	2808	CTCGTGGGTACTACATAAACCAATGGAACAAGCCACGACGCAATTCGCCAGTCGCT	2867
Qy	2056	GCAACGACCGGACCTTAAGTACTAGATGTGTAATGTTCACTCTCGGTCGGTAAAGGCT	2115	Qy	3136	GCCCAATCAACCTTTTCATGCACTCCAAACGGCTTACAAAGCCAGCACCACTCGACTGAGTC	3195
Db	1788	GCAACGACCGGACCCGAAAGTCTTAGACGTCTGTGTTCTGTGCTGGTGAATGGAGT	1847	Db	2868	GCCCAACAGAGATCTTCATGCAAGGCAATGGCTTAAAGCCGGCTCCACTGACTTAAGCG	2927
Qy	2116	CGGGTGGCTCGTCAACAGAACATCTGCACTATTGCTCCCGGCAAGAACTGTT	2175	Qy	3196	TGTCAACCTTGACACCAAGATGGATGAGCTAGTAGCCAGCTGGCTGGAGAACACCCACAA	3255
Db	1848	GGCGGTGGCATCCTCCAGAACAAACATTTGCACTTTTGTACCGGGCAAGAACTGTT	1907	Db	2928	CGTGACACTCACCCCAAGTTGGAGAGCTTGTGCAACGAGCTGGCCGAGAACACTCACAA	2987
Qy	2176	GCTGCAAACTGGCTTGTAGATCACGTATCTAGTCTCGTCCGAAACATCTTGGTGGCG	2235	Qy	3256	CTTTTGGCGCAGGAGAGGATACAGAGGATGGAATTAAGGACTTAATAGAGACTCGGA	3315
Db	1908	GCTACAGAGCTCTGTGTGACCATGTGGCGAGCATCCGACCGAACATCTTGTGGGTG	1967	Db	2988	TTTGTGGGCAACGGAGCGCATCCAGCAGGGTTGGAATTTATGCTCTGAACGAGGATAGTA	3047
Qy	2236	AGTAGAAGGTGGCAGTGTACCGAAATTTGTAATTCGAGGTGACTATGGAACACATAGA	2295	Qy	3316	CATGCATCGATCCCGCACCTGGTGCCATCCCGAAGTTGACGATGCCATCAAGAAGGC	3375
Db	1968	CGTGGACGTTCTTCATGTACCAAGTGGTACTTCGAGGTGACCATGGATCACATCGA	2027	Db	3048	AAACACACAGGAGTCCACACTTGGTGCCATATGCCAAAGTGGACGAGGCTATCAAGAAGC	3107
Qy	2296	GAAACCAACATATGATGCCATCTACGCATAGATGSGCTAACACTACTGTTATGT	2355	Qy	3376	CAACAGGACACAGCTCGGAGACTGTGAGGACCTGTGGTCTTACGGGTATATGCTGGA	3435
Db	2028	ACAGACCAACGCAATGATGCCCACTGCGCATTTGCTGGGCTAACTTCCGGGTATGT	2087	Db	3108	CAACAGGAGACAGCGTGGAGACAGTGGCAAGCTCTCTGTTTACGGATATGCTTGA	3167
Qy	2356	CCCATACCGGGTGGTGGAGAGTGGGAGTAAAGCGTGGGAGAGACCTGTGACTC	2415	Qy	3436	CCCGCTTACTGGGAGCAGCATGAAGCACTCTTGTGGAAGCGGTCAAAACAGAAAGCAAGC	3495
Db	2088	ACCGTATCCCGAGGCGGCAAGAGTGGGTGGCAATGGAATGAGGATGAGCGATGACCTGT	2147	Db	3168	TCCTCCGACCGGCGAAGGAAACGGAGGCACTTCTGGCCGAGGCAACCGCTCAAGTTCCG	3227
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Db	2148	CTTTGGATTTGATGGTGCCTTTCTTTGGACGGAGGTTCGCAAAACACTAGTGGTGGACG	2207	Db	3228	CGGATTCGGGACTTACAGGGTGGAGCGCAACTACGCCGTGACATCGGGCAAGTGGTACTT	3287
Qy	2476	TCATGCTGAAGCCCTTATTAAGAAAGTGAAGTGAAGTGTGATGTTGCAATGGAACCTGAC	2535	Qy	3556	CGAGTTTCAGATCTTAACGGCTGGACCTATGAGGCTGGCTGGGCTCACGCTGATATGCG	3615
Db	2208	GCTGCCGAGGAGCCCTTATTCGTTAAAGCGCATGTTATTGGGCTTGGCATTTGACCTTTC	2267	Db	3288	CGAATTCGAGGTCTCACGTCGGAACCAATGCGAGTGGGTGGGACACGGGCCGATGCTA	3347
Qy	2536	GGTACCCATCATCACTCATGTTCACCGAGTGGCGGTGACGGGATCTTCAACCACTT	2595	Qy	3616	ACCAGGAATGATGCTCGGACAAAGACGAGAACTCTCTGGGCTTTGATGTTTCAATAGAGA	3675
				Db	3348	TCGCGGAGCGATGCTGGGCGAGGAGCACACGATTTGGGCTTCGATGGACACAAATGTCAG	3407



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Db 3408 CAAAATGACCCCGATGATCAATGAGCACTTCGGAGTCGGTATGAGGTCGGCGATGTCAT 3467
Qy 3736 GGGGGTGTCTAGATCTCATTTGATAAGCAGATAAGTTTCTCACTCAACGGTGAAGTTGTT 3795
Db 3468 TGGTTGTTTCATCGATGTCAAGGAGCAACCGATCAGCTTCTCGTTGAACGGAGAACTCCT 3527
Qy 3796 GATCGATGCTCTTGGCGGAGAGACTACGTTTTCGTGATGT-----CAGGGTGACAACTT 3849
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Db 3588 CGTCCCGCGCTGCACCTCGGGAGTGGGCCAAGAGCGCGCTCATCTACGCCACAGGACGT 3647
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Qy 3970 CAATATGAAGAGAGACGTGACTACTGTGTACACCAAGACAGCCGATCTTTCGAGATAAC 4029
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Db 3768 CGAGGAGATGCCGACTGCGCATCGATGTACCCCGGATTCGCGCGCGCGCACACCC 3827
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Db 4008 TGCCCAATGAGGTCAGACACAGGCGCCCAATGAGCACATGTTGAAGGTGGCTT 4067
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Db 4068 CAATATGAACGACATCAAGGCGTTGACCCGTAAATTTTCGATGAGCACGCGGATGCTGAGGC 4127
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Db 4188 AACCTTCGAAACAGACA 4204
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RESULT 7
US-11-097-143-22562
; Sequence 22562, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22562
; LENGTH: 15606
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-22562
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Query Match 43.2%; Score 2158.2; DB 13; Length 15606;  
Best Local Similarity 70.8%; Pred. No. 0;  
Matches 2944; Conservative 0; Mismatches 1173; Indels 42; Gaps 4;

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Db 61 GGCAACCGGCACCTGCTTCTGAGAAATATTGCCGCAAAAGAACATGTCGCCGCCGATCTTTCG 120
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Db 181 GCGCGAGGATCCGAGACT-----GGCAAGGACCCGATTCGGACACAGG 225
Qy 554 ACCTACTATACGGCAATGCTATTTTTCGACATCTTAAACAGTGTATGTACTTCGCC 613
Db 226 ACATTGCTCTATGGCAATGCCATTTTGTGCGGTACCAACACAGTGTATGTACTTGCA 285
Qy 614 TGCTGTCAACATCATCATCCAGGATAAGCTGCCCTTTGACGTGGTCTGCAACAGCAC 673
Db 286 TGTCTGTCCACCTCTCGTCGAACGACAGCTGTCTCTTCGACGTGGGCTTCGACGAGCAC 345
Qy 674 TCCCAAGGTGAACCTGCTCGTGGACCCCTGCATCTCCAGCAAAACAGAGATCCGAGGC 733
Db 346 AGCCAGGAGAGGCTTGTGTTGGACGGTTTCATCCGCGAGAGCAAGACGCTCTGAGGC 405
Qy 734 GAGAAAGTGCAGTCCGAGATGACTTGTATCTAGTCTCCGTGGCCATTTGAGAGATACTTG 793
Db 406 GAGAAAGTGCAGTCCGAGATGATCTGTCTGTTGCTGCGTGGCCACCGAACGTTATTG 465
Qy 794 CACAAACGAAAGAGAACGAAAGTATCGATAGTGAACGCGTTCCTCCAGCGACACTGG 853
Db 466 CATACGACCAAGGAGAACGAAACAGTCTATTGTAAATCCAGCTTCTCATGTGACCCACTGG 525
Qy 854 TCGGTACAGCCCTATGCTACTTGGTATATCGAGGATGAAGTATGTGGCTATGCTTCGGA 913
Db 526 TCGGTGAGCCCTACCGCAACGGGCATCTCCAGGATGAAGTACGTGGGCTATGTCTTTGGC 585
Qy 914 GGTGATGCTCAGTGTCTTCCATGGAGGTGAACAGTGTCTCACTATACCTAGCACTGG 973
Db 586 GGCATGTGCTGCGTTTCTTCATGGTGGCGACGAGTGCCTGACCAACCGAGTACATGG 645
Qy 974 ACAAGGATGGGGGCAAAATATCGTAGTCTAACAAAGAGGTTTCAGTGA TGTCTCAAGCC 1033
Db 646 GGTGCTGAGGCGGACAAATATTGTTATTACGAGGCGCGTGGTTCATGGCACAGGCG 705
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1034 QY CTTTCTCTATGGCGCTGGAGCTGGCTAGAAACAAAGTGGCGGAGGTTTCATTAACCTGG 1093  
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 706 Db AGGTCCCTCTGGCGCTGGAACTCGCTCGAACCAAGTGGAGCTGGTGTATCAACTGG 765  
 1094 QY TACCATCTATGAGGATTCGGACATCACTACTGGAAGATATCTTGGAGTTAACGACCAG 1153  
 Db |||||  
 766 Db TACCACCGCATCGCATACGCACATAAACCACTGGACGCTACTTGGCGGTCAACGACAGC 825  
 1154 QY AATGAGCTGATTTAGTTAGCAGAGAGAACCCACAAACAGCTTCCTGTGCTTCTGCTG 1213  
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 826 Db AACGAACCTGATTCATAGTTAAGAGAGAGGCTTCGATTCACACAGCACTTCTGCTG 885  
 1214 QY CGCCAGGAGAGGATGATCAGAAAGCAAGTGTAGAGACAAAGCACTTGGAGGTCTATAGGC 1273  
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 886 Db CGGCAGGAGAAAGGA CGACGAGAAAGGTCTGGAGGACAAAGCACTTGGAGGTATCGGC 945  
 1274 QY GCGCCCATCATCAAGTACGGTACCTCCACCGTCACTTGTGAGCAGCATTCGGAGACTGGCTTG 1333  
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 946 Db TCGCCGATCATCAAGTACGGCGACACTACCGTCACTCGTTTCAGCACTCGGAGACTAGCTTG 1005  
 1334 QY TGGCTGTCTTATAAGCTTTACAAACGAGAGAAAGCGTGGGTAAAGTAGAAGAGAG 1393  
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 1006 Db TGGCTCAGCTACAAGAGTTTATGAGACGAAAGAGAGGCGGTAGGAAAGGTGGAGAGAG 1065  
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 Db |||||  
 1066 Db CAAGCGATTCCTCAAGAGGAGGCAAGATGGAACGATGGCTCGACCTCTCCAGGTACAG 1125  
 1454 QY GAGGAGAAATCTATGATCTCGAGTTATCAGAAAGTGTCTTCCGCTGTCTACTAAGTTT 1513  
 Db |||||  
 1126 Db GAGGAGGAGTCCAAGACAGCTCGTGTCACTCCGCAAGTGCAGCAGCTCTTCAACCCAGTTT 1185  
 1514 QY ATCAATGGCTGGAACCTTCAAGAGAACCGTCTGCTCACTCGATGTTCTTCCGCTCAGTG 1573  
 Db |||||  
 1186 Db ATTACAGCCTTGGAAACACTGACAGTCAAAATCGCCGACACTCCATTTTCTTCCAAAAGTTC 1245  
 1574 QY AACCTGGGCGAGATGGTGATGTCTTGAAGATCTCACCAACTACTTGCACAGCCCGAT 1633  
 Db |||||  
 1246 Db AACCTCAACGAGATGGTCAATGTCTTGGAGCTTGAATTAATCTATTTTTCGCAACCCGAA 1305  
 1634 QY GAGGATATGGAA CACGAGAAAGCAAAACAAATTCGCGCCCTCCGCAACCGTCAAGAC 1693  
 Db |||||  
 1306 Db GACGATATGGACACGAGGAGAAACAGAACCGATTCGCTGCGCTCGCAACCGACAGGAT 1365  
 1694 QY CTGTTCCAAAGAGAGGACATCTGAACCTGATCTCTGGAAGCTATAGACAGAGATCAACGTC 1753  
 Db |||||  
 1366 Db CTGTTCCAGGAGGAGGCGTGCTCAATCTGATCTCTGGAGGCCATTTGACAAGATCAACATA 1425  
 1754 QY GTACGCTCCAGGGGTTCTGGCTGGATTCCTGGCGGAGAGCAATCTGGACAGAGCTGG 1813  
 Db |||||  
 1426 Db ATCACTCCAGGGCTTCTAGCAGCTTCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485  
 1814 QY GAAATGATATCTGGATATTTGATCAGTTGCTGGCGGCAATATAAAGGCAACACACAG 1873  
 Db |||||  
 1486 Db GATCTCATCTCCACCTATTTGATACCAACTCTTGGCGGCCATCATCAAGGCAACACACAG 1545  
 1874 QY AACTGGCGCAGTTTCGCAACTCGAAACCGGTTCAACTGGCTGTCTTGGCGGCTCGGCTCG 1933  
 Db |||||  
 1546 Db AACTGGCGCAGTTTCGCAACAGTAAACCGACTCAACTGGCTATCTTCCGCGCTCGGTTCC 1605  
 1934 QY CAGGCTCGGCGAGGACCGGCACTGCTGACGCTGCTGCACTGGATCTCATCTGACTCG 1993  
 Db |||||  
 1606 Db CAGGCTCGAGGAGGGTTCCGGCATGTTGGACGCTACTTCACTCGGTGCTGATCAATTCG 1665  
 1994 QY CTTGAAGCGCTCAATATGATAGGAGCAACACATAAAAGTGAATATCTCTATTTAGAA 2053  
 Db |||||  
 1666 Db CAGAGGCACTAAACATGATCGGGATGAGCACAACAGGTGATCATCTCCCTGCTGGAG 1725  
 2054 QY AAGCAGGACGCGACCTTAAAGTACTAGATGTGCTATGTTCATCTCTGCTCGGTCAACGCG 2113  
 Db |||||  
 1726 Db AAGCAGGACGAGGACCCGAAAGTCTTAGACGTTCTGTGTTCTTGTGCTGGGTAAATGGA 1785

2114 QY GTCCGGTGGCTCGTCAACAGAAACAACATCTGCGACTATTTTGTGCTGCCGCGCAAGAACCTG 2173  
 Db |||||  
 1786 Db GTGGCGGTGGCATCTCTCCAGAAACAATTTGCGACTTTTGTCTACCCGGGCAAGAATCTG 1845  
 2174 QY TTGCTGCAAACTGCGCTTGTAGATCAGTATCTAGTGTCCGTCCGAAACATCTTCTGTGGGC 2233  
 Db |||||  
 1846 Db TTGCTACAGACGCTCTCTGGTGAACATGTGCGCAGCATCCGACCGAAACATCTTCTGTGGGT 1905  
 2234 QY CGAGTAGAAGGGTCCGAGTGTACCGCAATTTGGTATCTTTCGAGGTGACTATGGAACACATA 2293  
 Db |||||  
 1906 Db CGCGTGGACGGTCTTCCATGTACCAAGTGGTACTTTCGAGGTGACCATGCGATCACATC 1965  
 2294 QY GAGAAGACCAACATATGATGCCACATCTACGATAGGATGGCTTAACACTACTCTGTTAT 2353  
 Db |||||  
 1966 Db GAAACAGACCAACGATGATGCCACCTGCGCATTTGGCTGGGCTAACTATTTCCGGGTAT 2025  
 2354 QY GTCCCATACCGGGTGGTGAAGTGGGAGTAAACGCGTGGGAGACGACCTGTAC 2413  
 Db |||||  
 2026 Db GTACCGTATCCGGAGCGGCAAGTGGGGTGGCAATGGAGTAGGCGATGACCTGTAC 2085  
 2414 QY TCGTACGGGTTTGATGGCGCTTCTCTGTCTCCGCGGAGGAAACGCCGCTCAATAGG 2473  
 Db |||||  
 2086 Db TCCCTTGGATTTGATGGTCCCTTCTTTCGAGCGGAGGTCCGAAACACTAGTGGTGAC 2145  
 2474 QY ACTCATGCTGAAGAGCCTTATATAGGAAAGGTGACGTGATAGTGTGTCATTTGACCTG 2533  
 Db |||||  
 2146 Db CGCTGCCGAGGAGGCCCTTATCCGTAAAGCGATGTTATTTGGCGTTGCCATTCACCTT 2205  
 2534 QY ACGGTACCCATCATCACTTCACTGTTCAACGAGTGGCGGTGACGGGATCTTTCACCAAC 2593  
 Db |||||  
 2206 Db TCTGTGCCCATCATCACGTTTACTTTTAAACGAGTAAAGTGGCGGTAGCTTTTAGGAC 2265  
 2594 QY TTCAATCTGGAAGGATGTTCTTCCGGTCACTAGCTCTCTAGTAAAGCTGAGTTGTGG 2653  
 Db |||||  
 2266 Db TTTAACTGGAGGAAATGTTCTTCCGCTGATGATGCTCATCAAAACTAAGCTGTGCG 2325  
 2654 QY TTCTGTGGCGGAGAAACGCTAGACTCGGCTACGCGGTCCAGAGGCTTCTCCCG 2713  
 Db |||||  
 2326 Db TTCTTTTCGAGGATGATCATGGTCTTTAAAGTTTGGCCCGCCCATGGGATCTCTGCG 2385  
 2714 QY CTGTTGAGTCTCTCTGCGCAGCAGATCTCAGCTGGAGCGCTGCTTCTACTTCCGCG 2773  
 2386 Db CTGCTGAGTGTCTCATGCCGAGCAGATCTCAGTCTGGATCTTGTCTTCTACTTTGTT 2445  
 2774 QY AACCTGTCCAAGCGGCTTGGCTGAGCCCGCTAGTACAGGACGATACGCGCTTTTGTG 2833  
 Db |||||  
 2446 Db AATCTGCAAGAAATGTTTGGCGGACCATGGCTTATTTGAGGACGACACTGCTTTGTT 2505  
 2834 QY CTAAGCTGTGATCTTTACAGATTAATCTGCTGCTACATATGTGGAAACAAATCAGAGAC 2893  
 Db |||||  
 2506 Db CGAAGCCGTTGATACACCGGTGTGACATTTGCCAAGTTCTGTGGAACCAATCAAGGAG 2565  
 2894 QY AAGCTAGTGAATATTTACGAAATGTGGCTATGAATAGATCGAAGCAGCTGGATG 2953  
 Db |||||  
 2566 Db AAGCTGGCGGAGAAATATCCAGAGATGTGGGCTTAAACCAAACTGAGCGGCGGTGCTG 2625  
 2954 QY TACGCGACCAAGAGAGAGACTTGCACAAAGATCCACCCCTGCTGCTGCTTCCGAGCGA 3013  
 Db |||||  
 2626 Db TGGCGGAGACCGAGATGATACACCGCATCCATCTTGGCTCACCCATTTTCGAGAAG 2685  
 3014 QY CTCGCGCGCTGAGAAACGATACGATATACAATTTGTGTGTGACAGACTCAAGACTATC 3073  
 Db |||||  
 2686 Db CTTCGCGCGGAGAAAGGATACGACAACTCAACTAGCTGTGCAAAACGCTGAAGACGATT 2745  
 3074 QY CTGGCTCTGGGCTACTACATCAGCTTAGATTAAGCTTCCAGCAGCATCGGCAACCTTCT 3133  
 Db |||||  
 2746 Db ATCTGCTGGGATACTACATAACCATGGAACGACCAAGCAGCATGTCGCCAGCTGGCG 2805  
 3134 QY CTGCCCCAATGACCTTTCATGCGAGTCCAAACGCTCAAGAGCAGCACCCTCGACCTGAGT 3193  
 Db |||||  
 2806 Db GTGCCCAACGAGATCTTATGCGAGGCAATGGCTAAGAGCCGGCTCCACTTGCACCTAAGC 2865  
 3194 QY GCTGTCACTCGACACCCCAAGATGATGAGCTAGTAGGCTAGTGGCTGAGTGAAGAACCCAC 3253

Db 2866 GCGGTGACATCAACCCCAAGTTGGAGAGCTTGTGGACGAGCTGGCCGAGNACACTCAC 2925  
Qy 3254 AACCTTTGGGCCAGGAGAGATACAGCAGGATGGAATACCGACTTAATAGGACTCG 3313  
Db 2926 AATCTGTGGGCA CGGAGCGCATCAGCAGGTTGGACTTATGCTCTGAACGAGGATAGT 2985  
Qy 3314 GACATGATCGATCCCGCACCTGGTGCATACCGAAGTTGACGATGACCATCAAGAAG 3373  
Db 2986 GAAACACACAGGAGTCCACACTTGGTGCCATATGCCAAAGTGGACGAGGCTATCAAGAAG 3045  
Qy 3374 GCCAACAGGACACAGCCTCGGAGACTGTGAGGACCTCTGGTCTACGGGTATATGCTG 3433  
Db 3046 GCCAACAGGACACAGCGTGGAGACAGTGGCAAGCTCTGGTTTACGGATATGCTTG 3105  
Qy 3434 GACCCGCTACTGGGGAGCAGCATGAAGCACTCTGTTGGAGCGTCAAAACAGAACAA 3493  
Db 3106 GATCTCCGACTGGCGAAGAAACGAGGCACTTCTGGCCGAGGACAAACGCTCAAGTTC 3165  
Qy 3494 GCCGACTTCAGAAATACCGGCTGAGAGNACTATGCCGTGACTCTGGGAGTGGTAC 3553  
Db 3166 GCCGGAATCCGGACTTACAGGCTGGAGCGCAACTACCGCGTGA CATCGGGCAAGTGGTAC 3225  
Qy 3554 TTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTGGGCTCGGCTCACTGATATG 3613  
Db 3226 TTCGAATTCGAGGCTCTCACGTCGGACCAATGCGAGTGGTGGGACGCGCGATGTC 3285  
Qy 3614 GCACGAGAAATGATGCTCGGACAGAGCAAGTCTCTGGGCTTTTGATGTTACAATGAG 3673  
Db 3286 TATCGGAGCGATGCTGGGACGCGAGCACACCAAGTTGGGCTTCGATGGACACAATGTG 3345  
Qy 3674 GAAAGTGTACAGGGTAACTAGTCTTTCGGCAAGCAATGGCTGTGGTGGTACGTA 3733  
Db 3346 ACCAAAATGCAAGCGCGGATTCATTTGAGCACTTCGGAGTGGGATGAGGCTGGCGATGTC 3405  
Qy 3734 GTGGGGGTGTTCTTAGATCTCATTTAAGAACGATAAGTTTCTCACTCAACGGTGAAGTTG 3793  
Db 3406 ATTGGTGTTCATCGATGTCAGAGGACAAACGATCAGTCTCTGTTGACGGAGACTC 3465  
Qy 3794 TTGATGATGCTCTTGGCGGAGAGACTACGTTTCTGATGT- - - - -CCAGGGTGA CAAC 3847  
Db 3466 CTGATGAGCGGCTGGGCGGAGACGACACTTTGCCGACGTAAACCGCGAGGGGTGGC 3525  
Qy 3848 TTTGTACTGTTGACGCTTGTGTGTCGGCCAAAGCCAGGTTAAATACGTTCAAGAC 3907  
Db 3526 TTCGTGCCGCTGCACCCCTGGGAGTGGGCGAGAGGCGGCCCTCATCTACGGCCAGAC 3585  
Qy 3908 GTGAACACGCTGAATACTTCAACACTGTGCTCTGAGGAGGATATGAACCACTTCTGT 3967  
Db 3586 GTGGACTCACTCAAGTCTTCAACACTGTGCTCTGAGGAGGATACGAGCCGTTCTGC 3645  
Qy 3968 GTCAATATGAAGAGAGACGTAACCTCACTGGTACACCAAGACCGGATCTTCGAGAT 4027  
Db 3646 GTGAACATGCGCCGCGTTTACCACTGTTACCAAGGACGACCCATTTTGAAGAC 3705  
Qy 4028 ACGGATGAGATGATCGACACAGAAATAGATGTGACAGGATACAGCTGTTTCAGATACA 4087  
Db 3706 ACCGAGGAGATGCCGACTGCGCATCGATGTCAACCGGATTTCCCGCGGCGCCGACAC 3765  
Qy 4088 CCTCCATGCTCAAGATTTCCCAACACGTTTGGAGACGATGGAGAAAGCTTAACTGGGAG 4147  
Db 3766 CCGCGCACTTAAGATCTCGCAACACCTTCGAGACCATGGAGAGGCCCACTGGGAG 3825  
Qy 4148 TTTCTACGCTCTCACTGCTGTCTATCTGCCATAACGAGTTTCAATGACGAGGAGAAAA 4207  
Db 3826 TTTCTGCGTCTTTCCCTGCGGCTGACCTGATGGTGAGTTTATCAGCGAACAGGAGAG 3885  
Qy 4208 GCCAGGCTTGGGTAGAAATCAAGGACCGCCAAACGATCCTTAATGAAGAGGAGTTGAA 4267  
Db 3886 GCCAGACGCTGGGACGAGATTAAGAAACCGGAGTACCGACTGATGCGCGAGGCGGAGATC 3945  
Qy 4268 GCT- - - - -CAGATGTCGCCCATATTTGACCAAGATCATCAGGAGCGGT 4309

Db 3946 GCTGCCAAATGAGGTCCAGACACAGGCGGCCCCACATGACCAATGTTTAAAGTGGC 4005  
Qy 4310 TTCACCATGAACGATATTAAGGTTTGCACTACGAAGCAATCAGGAAGAGTTGCCAGC 4369  
Db 4006 TTCATATGAACGACATCAAGGCTTGACCCGTAATTTCCATGAGCAACGCGGATGCTGAG 4065  
Qy 4370 TC- - -CAAGATGAAGCGCTTCCAAAGGCCACCAAGGATCCATGACAAAGAGT 4426  
Db 4066 GCAGATCAATGATGCGGAGCCCAACCGTCCGCTCGCAAGGATCGCTCACCCGCAAC 4125  
Qy 4427 GTTACTATACAAAATTACA 4445  
Db 4126 ATAACCTTCGAAACAGACA 4144

RESULT 8  
US-10-668-767-7  
; Sequence 7, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Guttridge, Steven  
; APPLICANT: Rauh, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: BB1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 15413  
; TYPE: DNA  
; ORGANISM: Peregrinus falco  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1264)  
; OTHER INFORMATION: n = a,c,g, or t  
; FEATURE: CDS  
; NAME/KEY: (15397)  
; LOCATION: (17).. (15397)  
; OTHER INFORMATION:  
US-10-668-767-7

Query Match 41.6%; Score 2078.2; DB 8; Length 15413;  
Best Local Similarity 66.5%; Pred. No. 0;  
Matches 3172; Conservative 1; Mismatches 1475; Indels 120; Gaps 9;

Qy 266 GGGGAGCAAGCCGAGGAGGAGTGTGCTGCTGCGGAGGATGTTGGTAAACCGTCAT 325  
Db 29 GAGGTTGGATCTGAGCAGGATGATGTTTCTTCTTGAACGAGGATGTTGTTCTG 88  
Qy 326 TCGTGCACAGCAGCAGGAGGAGGAGTGTGCTGCTGCGGAGGATCTCGGCAACCGGAC 385  
Db 89 TCATGTACAGCCACCGGTGAAAGAGTGTGCTGCTGAGAGGATTTGGTAAACCGTCAT 148  
Qy 386 TGCTTCTCGAGAAATATGCGGACAGAAATACCGCTGATCTGTCGAGTGTGTTT 445  
Db 149 TGTTTCTGGAACATCATCGCTGACAGAAATATTTCCACAGATTTGTCCATGTGTTT 208  
Qy 446 GTCATCAACAGGCGCTTTTCAAGAGCTTTACAGGAGTTGGTAAACAGCTGCCGGATCT 505  
Db 209 GTTATTGAGCAAGCTTTATCGTTTCGAGCTCTTCAGAAATGGTTACTGCTGCTGGATCA 268  
Qy 506 GAAACTGGGAAAGAAACTTAGGTAAAGGATCCGGTTTCTGGTTATCGTACGCTACTATAC 565

Db 269 GAA-----GAGGGTAAAGGAACTGGATCAGGACATAGGACCCCTATTGTAC 313  
Qy 566 GCGAATGCTATTCTTTTCGCAATCTTAAACAGTGATATGTACCTGGCCCTGCTGTCAACA 625  
Db 314 GCGAATGCTATTCTCTCGGATCAAAACAGTGATATGTACTTGGCCCTGCTGTCAACC 373  
Qy 626 TCATCATCCAGGATAAGCTGGCTTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAA 685  
Db 374 AGCTCATCCAATGATAAATCTGTCATTTCGATGTGTGCTCTCCAAGAACATTCACAGGTGAG 433  
Qy 686 GCCTCTGCTGGTGAACCTCGATCTCTGCGAGCAAAACAGAGATCGAGGGCGAGAGGTGCGA 745  
Db 434 GCCTGTGGTGGACTGTGCATCTCTGCTTCCAAGCAAAAGATCGAGGGGTGAGAGGTGCGA 493  
Qy 746 GTCGAGAGTACTTCAATCTAGTCTCGGTGGCCATTTGAGAGATACCTGCACACACGAAA 805  
Db 494 GTTGTGACACTTGTATCTTAGTTTCACTTGGTGGCACTGAAACGATCTTGCAACACAAA 553  
Qy 806 GAGAACGAAGTATCGATAGTAAACGCGTCTTCCACGTGACGCACTGGTCCGTTACAGCCC 865  
Db 554 GAGAACGATTTGTCATCGTGAATGCTTCTTTCATGTAACTCATTTGCTCCGTTCCAGCCT 613  
Qy 866 TATGTACTGTGATATACGAGATGAAGTATGTGGGCTATGTTCGAGAGGTGATGTGCTC 925  
Db 614 TATGCCACAGGAATAAGTCGATGAAATATGTGGTTATGTGTTTGGTGGCGATGTGCTT 673  
Qy 926 AGGTTCTTCCATGGAGGTGACAGGTGCTCACTATACCTAGCACTTGGACAAAGATGGG 985  
Db 674 CGGTTCTTTCATGGTGGTGTAGTGGCTTCAATTCATCAACGTGGAGTGAAGCACCT 733  
Qy 986 GGGCAAAATATCGTAGTCTCAAAAGGAGTTCAAGTGTCTCAAGCCCGTTCTCATGG 1045  
Db 734 GGACAGATATGTGTTTATGAGGGAGGAGTGTGATGAGTCAAGCTGCTTCATTATGG 793  
Qy 1046 CGCTGGAGCTGGCTAGAACCAAGTGGGCGGAGGTTTCATTAACCTGTTGATCCCTATG 1105  
Db 794 AGACTAGAACTTGTCTAGAACAAATGGGCGAGGTGTTTCATAAAATGGTATCCACCCTAATG 853  
Qy 1106 AGGATTCCGCACATCACTACTCTGGAAGTATCTTGGAGTTTACGACCAAGATGAGCTGAT 1165  
Db 854 AGAATACGACACTTGACCACTGGTTCGATACCTTGGTGTCAAGCAACAAATGAATACAT 913  
Qy 1166 TTAGTTAGCAGAGAGAAACCCACACAGCTTCCCTGCTGCTTCTGCGCCGAGCAAGAG 1225  
Db 914 CTGATTGTGAGAGATGAGCAACGACGGCTGTGTCAGCATCTGTCTGGACACAGAGAA 973  
Qy 1226 GATGATCAGAAAGCAAGTGTAGAGACAAAGACTTGGAGGTTCATAGGCGCGCCCATATC 1285  
Db 974 GATGATCAGAAAGTGGTCTTGAAGACAAAGACCTAGAAAGTAAATAGGTGCACCAATTATC 1033  
Qy 1286 AAGTACGGTGAATCCACCGTCATTGTGACGATTCGGAGACTGGCTTGTGGCTGCTTAT 1345  
Db 1034 AAGTATGGTGAAGTACTGTTCTGTTGAGCAATTCGAGCTGGCTTGTGGCTTACATAC 1093  
Qy 1346 AAGTCTTACGAACCAAGAGAAAGCGTGGTAAAGTAGAAGAAAGCAAGCGATTCTC 1405  
Db 1094 AAATCATATGAACCTTAAAGAAAGAGAGTTGGAAGAGTTTGAAGAAACAAAGCTGTGCTC 1153  
Qy 1406 CACGAGGAAGGCAAGATGGAACGATGGCCCTCGACCTCTCCAGGTTCACAGGAGGAAGATCT 1465  
Db 1154 CATGAGGAAGAAAGATGGACGCGCTTGGATTCTCCCGCAGTCAAGAAAGAAATCG 1213  
Qy 1466 ATGACTGCTCGAGTTATACGGAAGTGTTCCTCGCTGTTTCACCTAAGTTTATCAATGGCCTG 1525  
Db 1214 CGTACCGCTCGTGTAAATAGGAAGTGTTCATCTCTTGTTCACCTCAGTTTATNAGAGGTCTA 1273  
Qy 1526 GAAACTCTTCAAGAGAACCGTCTGCTCACTCGATGTTCTTCGCGTCAAGTGAACCTGGCGAG 1585  
Db 1274 GAGACTTGCAGGTGAATAGAGGGCACTCGTTATTTTGTGCAACTGTGTAATTTGAATGAA 1333  
Qy 1586 ATGTTGTATGTCTTGAAGATCTCACCAACTACTCTCGCACGCCCGATGAGGATATGAA 1645  
Db 1334 ATGGTAAATGTGCTCGAAGATTGATTAACTATTTTGGCAGCCAGCAGATGATATGAA 1393

Qy 1646 CACGAAGAAAGCAAAACAAATTCGCGCCCTCCGCAACCGTCAAGSACCTGTTTCCAAGAG 1705  
Db 1394 CACGAAGAAAGCAAAACAAATAGTTCGTTCCGTTGAGAAATCGTCAAGATCTGTTTCAAGAA 1453  
Qy 1706 GAAGGCATATGAAACCTGATCTCGAAAGCTATAGCAAGATCAACGTCGTCAAGTCCAG 1765  
Db 1454 GAAGGCATATTAATTAATTTCTGGAAGCCATCGATAAAATAAATGTATCAACGTCTCAA 1513  
Qy 1766 GGGTTCCTGGCTGATTTCTGGCGGGAGAGAAATCTCGACAGAGCTGGGAAATGATATCT 1825  
Db 1514 GGATTCCT---TGTAAGTTTAGAGGAGATGAATCAGGACAAAGCTGGGATATAATTTCT 1570  
Qy 1826 GGATATTTGTATCATGTCTGGCGGCAATATAAAGGCAACCAACAGAACTGGCGGAG 1885  
Db 1571 GGTTACCTGTATCAATCTTCTGCTGATTAATTAAGGAAATCATACAAATTTGGGCTCAG 1630  
Qy 1886 TTCCGGAACCTCGAACCGGTTCAACTGGCTGTTCTCGGCCCTCGGCTCGCAGGCTCGGGC 1945  
Db 1631 TTTCGGAATTCAAATTCGTTGATTTGGCTGTTTCAGCAGACTGGGCTCACAAGCATCAAGT 1690  
Qy 1946 GAGGSCACCGCATGCTCGACGCTGTCACCTGCATCTCATCGACTCGCCTGAAAGCGCTC 2005  
Db 1691 GAAGGCAACGGGAATGCTTGTGATTTGCAATTTGCTTCTCATTTGCTTGCCTGAAAGCGTTG 1750  
Qy 2006 AATATGATGAGGGACGAACACATATAAAGTGTATAATCTCTTATTAGAAAGACACGGACGC 2065  
Db 1751 AATATGATGAGGATGAGCATATAAAGTTATAATATCTCTTCTTGAGAAACATGGAAGG 1810  
Qy 2066 GACCCTAAGATPACTAGATGTGCTATGTTCACTCTGCGTCCGTAACGGGCTCGCGTGGCG 2125  
Db 1811 GATCCGAAGTTTGGATGTTCTCTGTTCACTGTTGTGGGTAAATGGTGTGCTGTTGCT 1870  
Qy 2126 TCGTACAGAACACATCTCGACTATTGTCGTCGCCGCAAGAACCTGTTGCTGCAAACT 2185  
Db 1871 AGCTCAGAAACAAATATTGTGATTTCCCTTCTACTGGAAGAAATCTTCTTCTCAAAG 1930  
Qy 2186 CGCTTGTAGTACGCTATCTAGTGTCCGTCCGAACATCTTCTGGGCGGAGTAGAAGGG 2245  
Db 1931 CAACCTAGTGGATCATGTGGCTAGTGTCCGTCCTCAAAATATATTGTTGGCGGTGTTGCTGGC 1990  
Qy 2246 TCGGCAGTGTACCGCAATATGTTACTTCAGGTGATATGAGACCATATGAGAACACCA 2305  
Db 1991 TCTGCAGTTTATCAAAATATGTTATTTTGGGTTTACCATGATCACAATGAGCAGACACA 2050  
Qy 2306 CATATGATGCACATCTACGCATAGGATGGCTTAACACTACTGTTATGTGCCATPACCG 2365  
Db 2051 CACATGACACCTCACTTGAGAAATTTGGCTGGGCGAACACTAGTGGATATGTGCCCTTATCCT 2110  
Qy 2366 GGTGTTGTGAGAAAGTGGGAGGTAAACGGCTGGGAGACGACCTGTACTCTGTAACGGGTTT 2425  
Db 2111 GGAGGAGTGAAGAGTGGGTTGGAATGGAGTTGGTATGATCTTTATCTTATGCGGTTT 2170  
Qy 2426 GATGGCCTTACCTCTGCTCGGCGGAGGAGAACCCCGGTCAATAGGACTCATGCTGTA 2485  
Db 2171 GATGGCGGAATTTATGACAGAGGAGACGTAAACCTTGTGT---TCTACCGCATCGACT 2227  
Qy 2486 GAGCCTTATATTAGGAAGGTGACGTGATAGTTGTGCAATTTGGACTTGGACCTGAGCTACCAATC 2545  
Db 2228 GAGCCATTCATCAAGAAAGGCGATGTAATTTGGAGTGTCTCTAGATTTTAATCTGTGCCAATC 2287  
Qy 2546 ATCAACTTCATGTTCAACCGGAGTGGGTGACGGGATCTTTCACCAACCTTCAATCTGGA 2605  
Db 2288 ATAACATTTTCAATTCATGTTTCGCTTATAGGGGCTGCTTCAGAGATTTCAACTATGAT 2347  
Qy 2606 GGCATGTTCTTTCCCGGTCAATCAGTGTCTTATAGTAAAGTGTGAGTGTGCTGCTGGGC 2665  
Db 2348 GGAATGTTCTTTCTCTGTTATAAGTTGCTCGCACAAAGCTAAGTTGGCGATTTCTTTTAGGT 2407  
Qy 2666 GGAGAACACGGTAGATCCCGGTACCGGCTCCAGNAGGCTACTCCCGCTGGTGGAGTCT 2725  
Db 2408 GGAGACCA TGGTTCGACTGAAATATATGTTCCACAGAAAGATTTCTCTCCACTTGTGAAAGT 2467



Db 4562 TCTGGCAGTGAATTAATTCGGTGGCAACGAAATATTTCGATGGCGAATGCTCAAGTTG 4621  
 Qy 4913 ATCAATAGTACTTTTATGGAGTCAGGATCTACCCAGGTCAAGACCCCAACCAATGTAC 4972  
 Db 4622 ATCAATGAATATTTCTACGGTGGCGTATTTTCCCGGTGAGGTCCAACTCATGTGTAT 4681  
 Qy 4973 ATCGGCTGGGTGACCAACCCAGTACCCT 5000  
 Db 4682 GTCGGTGGGTGACAAACCCAGTACCCT 4709

RESULT 9

US-10-668-767-3  
 ; Sequence 3, Application US/10668767  
 ; Publication No. US20040171114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Caspar, Timothy  
 ; APPLICANT: Cordova, Daniel  
 ; APPLICANT: Gutteridge, Steven  
 ; APPLICANT: Rauh, James  
 ; APPLICANT: Smith, Rejane  
 ; APPLICANT: Tao, Yong  
 ; APPLICANT: Wu, Lihong  
 ; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
 ; FILE REFERENCE: BBI533 US NA  
 ; CURRENT APPLICATION NUMBER: US/10/668,767  
 ; PRIORITY FILING DATE: 2003-09-23  
 ; PRIOR APPLICATION NUMBER: 60/412,795  
 ; PRIOR FILING DATE: 2002-09-23  
 ; PRIOR APPLICATION NUMBER: 60/427,324  
 ; PRIOR FILING DATE: 2002-11-18  
 ; NUMBER OF SEQ ID NOS: 149  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 15845  
 ; TYPE: DNA  
 ; ORGANISM: Myzus persicae  
 ; FEATURE:  
 ; NAME/KEY: Unsure  
 ; LOCATION: (36)..(37)  
 ; OTHER INFORMATION: n = A, C, G, or T  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (5807)  
 ; OTHER INFORMATION: n = a or t  
 ; US-10-668-767-3

Query Match 36.9%; Score 1846; DB 8; Length 15845;  
 Best Local Similarity 63.3%; Pred. No. 0;  
 Matches 2988; Conservative 0; Mismatches 1685; Indels 51; Gaps 8;  
 Qy 278 GAGCAAGATGATGTTTCAATCTTGGCTACGGAAGACATGGTGTGCATGTCTGTCGACAGG 337  
 Db 301 GAACAGGACGATGCTCGTTTCTCCGAGCGGAAGATATGTTGTGTTTATCATGTACCGCG 360  
 Qy 338 ACAGGAGAGGGTGTGCTGCTCGGAGCTCTCGCAACCGGACCTGCTTCTCTGGAG 397  
 Db 361 ACCGAGAGAGAGTTTGTCTTGACGAGAGGATTTGGAATTCGGCATTTACTTAGAA 420  
 Qy 398 AATATTGCCCAAGAACATACCGCTGATCTGTGCGAGTGTGTGTTGTCTATCGAACAG 457  
 Db 421 AATATTGCCGATAGAAATATCCACCGATTTATCACAGTGTGTTTGTGTCATTGAACAA 480  
 Qy 458 GCGTTTTCAGTAAGAGCTTTACAGGAGTTGGTAACAGCTGCGGGATCTGAACCTGGAAA 517  
 Db 481 GCATTATCTGTAGGCGTTTACAAGAAATAGTGACAGCTGCAAGTTCTCAAGAGGAAAA 540  
 Qy 518 GAAACTTAGTAAGGTACCGTTCTGGTTATCGTACCTACTATACGGCAATGCTATT 577  
 Db 541 G-----GCGGAACCTGATCTGGACACCGGACGTTACTGTACGGAATGCTATT 588  
 Qy 578 CTTTTCGACATCTTAAACAGTGATGTACCTGGCGCTGCTCAACATCATCCTCCAG 637

Db 589 TTATTGCGTCATCAAAATAGTGATATATTTAGCTTGTCTATCAACAAGTTCCTCAAT 648  
 Qy 638 GATAAGCTGGCCTTTTGAGCTGGGCTGCAACAGACATCCCAAGGTGAAGCCTGTGTGG 697  
 Db 649 GATAAATTAATCTTTGAGCTGGTGTACAGAGCATTCACAAGGTGAAGCTGTGTGGTGG 708  
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 Db 709 ACTGTTTCATCTCGTCATCGAACCAACGATCAAGGGGTGAAGAAAGTTCCAGTCCGAGATGAT 768  
 Qy 758 TTGATTCTAGTCTCCGTCGTCATTGAGAGATCTTGCACACAAAGAAAGAAACGAAGTA 817  
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 Qy 818 TCGATAGTGAACGGCTGTTCCACGTGACGACCTGGTGGTACAGCCCTATGGTACTCGT 877  
 Db 829 TCTGTAGTAAATGCTCATTTTCACTGTAACCTATTGGTCAGTACAACCATATGGTACTCGT 888  
 Qy 878 ATATCGAGGATGAAGTATGTGGGCTATGTGTTCCGAGGTGATGTCTCAGGTTCTTCCAT 937  
 Db 889 ATCAGCAGAAATGAATACGTTGGTGTATGTGTTGGTGTGACGTACTAAGATTCTTTCAT 948  
 Qy 938 GGAGTGAACGAGTCTCTCACTATACCTAGCACTTGGACAAAGGATGGGGGCAAAATATC 997  
 Db 949 GCGCGGACGAGTGTGACAAATACCGTCGTCTGAGGACATGTTTCTGGACAAAATATA 1008  
 Qy 998 GTAGTCTACAAAGGAGGTTTCAGTGTCTCAAGCCCGTCTCTATGCGGCTCGAGCTG 1057  
 Db 1009 GTAAATTTATGAGCGGGAAGCGTTATGAGTCAACAGATCATTTATGCGGTTTGGAGTTG 1068  
 Qy 1058 GCTAGAACCAAGTGGGCGGAGGTTTCATTAACCTGGTACCATCTCTATGAGGATTCGGCAC 1117  
 Db 1069 GCTAGAACTAAATGGGCGGTTGCTTCAATTAATGGTACCATCCAAATCGAATAAGACAT 1128  
 Qy 1118 ATCACTACTGGAAGATATCTTGGAGTTAACCCAGATGAGCTGATTTAGTTAGCAGA 1177  
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 Qy 1178 GAGGAACCCACAAACAGCTTCTGTCGCTTCTGCGCCAGGAGGAAGATGATCAGAAAG 1237  
 Db 1189 GAAGAGCCACCATGTCATCTTACATTTTCTTACGCCCAAGAAAAGACGACCAAAAA 1248  
 Qy 1238 CAAGTGTTAGAAGACAAGGACTTGGAGGTCTAGCGCGCCCATCATCAAGTACGGTGAC 1297  
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 Db 1369 AAAAAAAGAGTGTGCGGTAAAGTAGAAGAAAACAAGCAGTATTACACGAAGAAGT 1428  
 Qy 1418 AAGATGGAACGATGGCTCGACCTCTCCAGGTCAAGGAGGAAGATCTATGACTGCTCGA 1477  
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 Db 1549 AGTAACAGCGGTTCGTCATTTATTTTGTTCATTCGTTAATCTTAATGAATGGTCATGTGT 1608  
 Qy 1598 CTTGAAGATCTCACCAACTACTTCGACAGCCCGATGAGGATATGGAAACGAAGAAAAG 1657  
 Db 1609 CTAGAAGATTTAAATAATTTACTTTTGTCTCAACCTGAAGAGGATATGGAGCAAGAAAAA 1668  
 Qy 1658 CAAAAAATTTCCGCGCCCTCCGCAACCGTCAAGGACCTGTTCCAAAGAGGAAGGCACTG 1717  
 Db 1669 CAAAAACCGATTTAGAGCATTAAGAAATAGACAAGATTTTATTCAAGAAAGAAAGAAATATTA 1728



Qy	1718	AACGTGATCCCTCGAAGCTATAGACAAGATCAACGTGCTCAGTCCGAGGGGTTCTCGCT	1777
Ds	1729	AATTTAAATCTTAGAAGCCATTTGATAAAAGTTAACTATATCATCATCTCAGGGATTCATGGTC	1788
Qy	1778	GGATTTCTGGGGGAGACGAATCTGGACAGAGCTGGGAATGATATCTGGATATTTGTAT	1837
Ds	1789	AGTT---TAGCCGGTGATGCTGGACAAAGTTGGATGTGAATTCCTGGTTATTTATAC	1845
Qy	1838	CAGTTTGTGGGGCAATAATAAAGGCCAACACACGAACCTGCGCGCAGTTTCGCAACTCG	1897
Ds	1846	CAGTTGTAGCTGCAATTAATTAAGGAAATCAACCAACTGTGCTCAATTTGCTAACT	1905
Qy	1898	AACCGGTTCAACTGGCTGTTCTCGCGCTCGGCTCGCAGGCTCGGGGAGGGCACC	1957
Ds	1906	AACCGATTAAATTTGGTTATTCAGCGGTTTAGGATCTCAAGCATCCAGTGAAGGAAC	1965
Qy	1958	ATGCTCGACGTGCTGCACTGCATCTCATCGACTCGCTGAAGCGCTCAATATGATGAGG	2017
Ds	1966	ATGTTAGATGCTTTCATTTGTTCTCATCGATTTCTCAGAGCTTTAAATATATGATGAAA	2025
Qy	2018	GACGAACACATAAAGTGATTAATCTCTATTAGAAAAGCACGCGACCCCTAAAGTA	2077
Ds	2026	GACGAACATATTAAGTTAATAATCACTTTTGGAAAAACATGCTGCTGATCCAAAGTG	2085
Qy	2078	CTAGATGCTATGTTTCACTCTCGCGTCGGTAAACGGCGTCGGGTCGGCTCGTACAGAAC	2137
Ds	2086	TTGGATGTTTATGTTCTCTGCTGTTGGTTAACGGTGTGCTGTAAAGATTGCGCAAAAT	2145
Qy	2138	AACATCTGCGACTATTGCTCGCCGCGAAGAACCTGTTGTCGCAACTGCGCTGTAGAT	2197
Ds	2146	AATATATGATGATTTCTTATTAAGAAAAAATTTACTTCTTCAACCTTACTTGTGAC	2205
Qy	2198	CACGTATCTAGTCTCGGTCGAAACATCTTCTGGGCGGAGTAGAAGGTCGGCAGTGATC	2257
Ds	2206	CACGTAGCGGACGTTACGTTCCCAATATTTTGTGTGCTCATGTAAGTGGATCTGCTTTAT	2265
Qy	2258	CGCAAAATGTTACTTCGAGGTGATATGACACATATAGAAAGACACACATATGATGCCA	2317
Ds	2266	AGAAAAATGTTATTAAGTTGGCAATAGATCATGTAGAACAACTACTCATTTAAATCCG	2325
Qy	2318	CATCTACGATAGATGGGCTTAACACTACTGTTATGTCCTATGTCCTACCCGGTGGTGAG	2377
Ds	2326	CACATTCGATTGAATGGGCAATACAGCTGTTATGTTTCCATATCTCTGGTGGTGAGAA	2385
Qy	2378	AAGTGGGAGGTAAACGGCTGGGAGACGACCTGACTCGTACGGGTTTGTAGCGCCCTAC	2437
Ds	2386	AAATGGGGCGAAGCGATTTGGGATAATTTATACITTTTGGATTTGATGGATCATAT	2445
Qy	2438	CTCTGTCGGCGGAGGAAGACCCCGGTCAATAGGACTCATGCTGAAGAGCCTTATATT	2497
Ds	2446	TTATGGACAGAGGACGTAAGTCAAGGAGT---GATGCCCGGAACACAAATTTCTAACAT	2502
Qy	2498	AGGAAAGTGACGTATAGTTGTGCAATGGACCTGACGATCCCATCATCACTTCATG	2557
Ds	2503	AAAAAAAGTGAATGATTTGGCTGTGCATTAACTTTAACTATTTAACTTTTACA	2562
Qy	2558	TTCAACGAGGTGCGGGTGAACGGGATCTTCAACCACTTCAATCTGGAAGGCATGTTCTTC	2617
Ds	2563	TTGAACGCTCAACTTGTCCAGGTGGCTTTAGAGACTTCAATTTAGATGGATGTTTTC	2622
Qy	2618	CCGCTCATGCTGCTTAGTAAGCTGATGTTGTCGGTTCCTGCTGGCGGAGAACACGGT	2677
Ds	2623	CCAGTAATTAGTTGTTCTCAAAAGTCAGTTGTGCTTTTTTATTTGGGTGAGATCAGGT	2682
Qy	2678	AGATCCGGTACGGCTCCAGAGGCTACTCCCGCTGGTGAGTCTCTCTCCGCCGAC	2737
Ds	2683	CGATTGAAGTTTACTCTCTCCAGAGCAATTTCTCCCTTATTGAAACCTTATTACCTCAA	2742
Qy	2738	CAGATCTCTCAGCTGGAGCCGTGCTTCTACTTCGGCAACCTGTCCAAAGCGGCGCTTGCT	2797
Ds	2743	CAAAATTTGCAATTTGATCCCTGTTTATTTTGGGAACCTTAATTAATGCTGCTCACG	2802

Qy	2798	GGACCCCGCTAGTACAGGACGATACGGCTTTTGTGCTACGCTGTGTGATCTTTACAG	2857
Ds	2803	GGTCCATGTTGTTGAGACGATGATGATTTGTTCCAAATCCAGTTGATCTTCATG	2862
Qy	2858	ATTACTCTGCCTACATATGTGGAAACAAATCAGAGACAAGCTAGCTGAAATAATTCAGAA	2917
Ds	2863	GTCACTTGCCTAGTTACATAGAAAATATTAAGACAATAATAGCAGAGAAATATTCAGAA	2922
Qy	2918	ATGTGGCTATGAATAAGATCGAAGCAGGCTGATGTACGGCCACGACGAGAGACTTG	2977
Ds	2923	ATGTGGCAATGAATAAATTTGAAGCTGTGGCAATATGGCGATAAAGAAATGATACT	2982
Qy	2978	CACAAGATCCACCCCTCGCTCGCTCGAGCGACTCCCGCGCTGAGAAACGATAC	3037
Ds	2983	AGGAAGTATCATCATGTTTAAATACAGTTTGACAAGTTGCTCAGCGGAGAGCGTTAT	3042
Qy	3038	GATATCAACTTCTGCTGTCAGACAACCTCAAGACTATCCTGGCTCTGGCTACTACATCAGC	3097
Ds	3043	GATTCCTCAATTAGCTGTGCAACCGCTTAAACCGTTATTGCGTTAGGTTATCACAATCT	3102
Qy	3098	TTAGATAAGCTCCAGCACGATCCCGAACGTTGCTGCTGCCAATGAACTTTTCATCGAG	3157
Ds	3103	ATTGATAATCCACGCTCCCGCATTTAAACAGTCCGGCTGCCAAACGAACTTTATGCAA	3162
Qy	3158	TCCAAAGGCTTACAAAGCAGCACCACTCGACTGAGTCTGTCACTCCCTGACACCCCAAGATG	3217
Ds	3163	TCCATGGATATTAACCAAGCACCACTAGATTTTATCTGCTATCATTTTGTCAAGNAATG	3222
Qy	3218	GATGAGCTAGTAGCCAGCTGGCTGAGAACCAACCAACCTTTTGGGCCAGGAGAGATA	3277
Ds	3223	GAAGAACTAATTCATCAGTTAGTCGGGAAATACACATACTATGGGCAAAAGAAATA	3282
Qy	3278	CAGCAGGATGGACTTACGCACTTAATGAGGATCTGGACATGATCGATCCCGCACTG	3337
Ds	3283	CAGCAAGGATGGACATATGGATTAATTAAGAAATTAACAATGTGGCAGTCTCATTTA	3342
Qy	3338	GTCCCATACCGAAGTTGACGATGCCATCAAGAGGCCAAACAGGGACACAGCTCCGAG	3397
Ds	3343	GTACCGTACAGAAAGTAGACGCTATTTAAAGAGCTAATAGAGATACAGCAAGCGAA	3402
Qy	3398	ACTGTAGGAGCCCTGCTGCTACGGGTATATGCTGGAACCCGCTACTGGGGAGCAGCAT	3457
Ds	3403	ACAGTCGCGACATTTATGGTATATGGTTACAAATTTAGATCCCGCACTGGAGAAACAAAC	3462
Qy	3458	GAAG---CACTCTGTTGGAGCGTCAAAACAGCAAGCAAGCCGCTTCAGAACATACCGC	3514
Ds	3463	GAAGCGACACTCTCTAAACAGATGAACTCTAATAGATATTTGACGTTTCAGAACATATCGT	3522
Qy	3515	GCTGAGAGAACTATGCGCTCAGCTCTGGGAAGTGGTACTTCGAGTTTGGATCTCTAACG	3574
Ds	3523	CGGAAAAAACGATGCGCTTCTAGTGGAAATGGTACTTCGAAATTTGAGATGACTGACA	3582
Qy	3575	GCTGGACCTATGAGGGTGGCTGGGCTCACGCTGATATGGCACCAAGGAATGATGCTCGGA	3634
Ds	3583	AGTGGACCTATGCGGGTGGATGGGCCAGGTTACATGTTTCCCGGGTTATCAAAATCGGC	3642
Qy	3635	CAAGACAGAACTCTCGGGCTTTTGTGTTTATGTTTCAATGAGAAAGTGTACAGCGGTAAAC	3694
Ds	3643	AGTGTGAAAAATTTCTGGGCAATTTGATGTTTATAACGAAAGAAAAATTTTATCATGGGACA	3702
Qy	3695	ACTGAGTCTTTTCGGCAAGCAATGGGCTGTTGGTGAACGTAGTGGGGGTGTTCTAGATCTC	3754
Ds	3703	GCCGAATCATTTGGTGAACAGTGGCAAGTTGGAGATGCTCGTGGAGTGTGTTTATGATTTA	3762
Qy	3755	ATTGATAAGACGATAAGTTTCTCATCTCAACCGGTGAGTTGTTGATGGAATGCTTTTGGCGGA	3814
Ds	3763	ATGGAACATACATTAAGCTTTTCGATGAACGGAGAAATTAATAATGATACGTTAGGAGGG	3822
Qy	3815	GAGACTACGTTGCTGATGTCAGGGTGACAACTTTGTACTGCTTGCACGCTTGGTGTGTC	3874
Ds	3823	GAACCAACATTTCTGAAGTCCAAGGAGAGGATTTGTACTCTGCTTTTACGCTGGGACTA	3882
Qy	3875	GGCAAAAAGCCAGGTTAAACATACGGGTGAGGACGTGAACACGCTGAAATACTTTCACAACA	3934

Db 3883 GGACAAAAGCAAAATTGACATTTGGTCAAGACGTTAACTCATTTGAAATACCTTCACGACT 3942  
Qy 3935 TGTGCTGTCAGAGGGATGAACCACTTCTGTGTCATATGAAGAGAGCTGACTCAC 3994  
Db 3943 TGTGACCTTCAAGAAGGATATGAACCACTTCTGTGTAATATGAAGAGCGCTGTGCTTAT 4002  
Qy 3995 TGGTACACCAAGACACAGCCGATCTTCGAGATACGGATAGAGATGATCGACACCAAGAATA 4054  
Db 4003 TGGTATCTAGGATCAACCAATTTTGGATATCTGACGA---TTTTCGTCTGTTAT 4059  
Qy 4055 GATGTACACGAGATACAGCTGGTTCAGATACACCTCCATGCTCAAGATTTCCACAAAC 4114  
Db 4060 GATGTTACAAAGATACCACTGGTTCAGATACACCACTTGTCTGAAGATAAGTCAATA 4119  
Qy 4115 AGTTTGTAGACATGAGAAAGCTAACTGGGAGTTCTTACGTCCTCTACTGCTGCTCATC 4174  
Db 4120 ACATTTGAAACCATGGAAGAACCAATTGGGAATTTTACGGCTATCATTTACCTGTCATA 4179  
Qy 4175 TGCCATAACGAGTTTATTGACAGGCAGAAAAGCCAGCGTTGGTAGAAAATCAAGGAC 4234  
Db 4180 TGTCTACCAAGTTTATTGGCGATCAAGAAAACAAAGGGGATGGCAAGAAATAGAATT 4239  
Qy 4235 CGCCAAACGGATCCTAATGAAAGAGGAGTTGAAGCTCAGATGCCGCCATATTACCAG 4294  
Db 4240 AGGCAACACAGGTTATTGCGCAATCTGAGCATGCT---ACTCTGCTCATATTGAACGA 4296  
Qy 4295 ATCATGAGAGGGGTTTCCATGAACGATATTAAGGTTTGCACACTACGAGACATACG 4354  
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Qy 4355 GAAGAGTTGCCAGCTCCAGATGAAGCGCTTCAAGGCCACCAAGTGAAGGATCC 4414  
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Qy 4415 ATGACAAGAGGTGTTACTATACAAAATTACAATAATTTGCAACCCAGGCCCAAGTCAACGCG 4474  
Db 4417 AATCAACACCAACCCACCCAGACCAACCAAGAGGGTCATTATCAGGCGATGACTTA 4476  
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Qy 4835 ATGACGACGAGCACTCTCGCGAGTCGGCTACGGAAACTGTGCGCAATGAGATCTTCGAT 4894  
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Qy 4895 GCAGAGTTGTAAGCTCATCAATGAGTACTTTTATGAGTCAAGATCTACCCAGGTCAA 4954  
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; Sequence 5, Application US/10668767  
; Publication No. US20040171114A1  
; GENERAL INFORMATION:  
; APPLICANT: Caspar, Timothy  
; APPLICANT: Cordova, Daniel  
; APPLICANT: Gutteridge, Steven  
; APPLICANT: Raun, James  
; APPLICANT: Smith, Rejane  
; APPLICANT: Tao, Yong  
; APPLICANT: Wu, Lihong  
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors  
; FILE REFERENCE: B1533 US NA  
; CURRENT APPLICATION NUMBER: US/10/668,767  
; PRIOR FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: 60/412,795  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: 60/427,324  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 15315  
; TYPE: DNA  
; ORGANISM: Periplaneta americana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(15312)  
; OTHER INFORMATION:  
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Query Match 36.7%; Score 1835.2; DB 8; Length 15315;  
Best Local Similarity 63.2%; Pred. No. 0;  
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Qy 326 TCGTCACAGCAGCAGGAGAGAGGCTGCTGGCTGCCAAGGCTTCGGCAACCGGCAC 385  
Db 73 TCATGCATCTGCACCTGGAGAAAGAGTTTGTCTTGACGCTGAAGGATTTGGAATCGGCAC 132  
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Db 133 TGTACTTTGGAATAATTTGCCGATAAAAATATTCCACCGACTTGTCTCAGTGTGTATTT 192  
Qy 446 GTCATCGAACAGCGCTTTTCAGTAAGAGCTTTACAGGAGTTGGTAAACAGCTCGGGATCT 505  
Db 193 GTCAATTGAACAAGCATTTATCAGTGAGAGCTTTTACAAGAACTAGTTTACAGCTACAAGTTCT 252  
Qy 506 GAACTCGGGAAGAAAACCTTAGGTAAGGTACCGTTCTGTTTATCGTACGCTACTATAC 565  
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3595 ACTCTGGGACTAGGACAAAGCAAAATTAATCTTTTGGTTCAGACGTAACCTCAATTGAAA 3654  
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3772 TCCTGTCTAAATGTGATGTTTACAAGAAATTCACGCTGTTTCAGATACACCACTGCTTAAAA 3831  
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4009 CATATTGAAACAAATATGAAATCAGGATTTTCAATGAGTATATAAAGGCTTTCATCGA 4068  
Qy  
4343 GAAGCAATCAAGGAGGTTGCCAGCTCCCAAGATGAAGAGGCTGCTTCAAGGCCACA 4402  
Db  
4069 GGTATTTCGGATGATCCTGTAGAAAACGATGAAATGATGCCAAACACATGCACTTTTACCA 4128  
Qy  
4403 CGTAAGGATCCATGACAGAGGTTTACTATACAAATTAACAAATTTGCAACCGAGC 4462  
Db  
4129 CCAAGAGGAAAAAATCAACCAACCCAGCAGCCACCAAGAAAGGCTTTTATCTAGA 4188  
Qy  
4463 CAAGTCAAGGCTGACCGGTCGACCAAGCTGAAGCTGAAATGGCCAAAGTATGACTTGGGA 4522  
Db  
4189 CACGATGACTTAA-----CGATCGAAATGACGGAAGTTGAAATCGTTCATCTAGT 4239  
Qy  
4523 GCGCAAGGTTTGAACGCTGATGAAGAGGACGAAGAGGGGACGATCGCTTTTCAAGTTC 4582  
Db  
4240 GAATTTGAATTTTAAATATATAATCAGCAAAACCGTAAATGGCCAGGACATAAACAAGAT 4299  
Qy  
4583 TTCAGAACGAGCGCGGCGGAAAGAGTATGCTGCTAAATCCGCTTAAATCCAAACACCA 4642  
Db  
4300 GACAGAAAAAAGAGGAGGCTTCTCCATTTTCGATTTTTCGAGAAAAAAGAGGGCT 4359  
Qy  
4643 GACCCCTTCAGTGATACCGAAAGTATACCAAGACGTTGCTCGAAGGCTTAAACCTCAG 4702  
Db  
4360 TCGGATAATCTTAAAGAGAGCAAAACTCCGATCCAGCTAGAAATGTGTTAGATCAGT 4419  
Qy  
4703 ATCAAGTGTACAGGCCAATCAAGATATAACCGCATGAACGCGCTCTAGCAGGACC 4762  
Db  
4420 AATGCTGTCTACAGACCTTAATACATTAATGAAGAAATACTCC---CCAAATTAAGAT 4475  
Qy  
4763 AACCTGTATGGAGGCCAAGTTGGTTGAACTCGAAGCGCTCAGATGGCGAGCCGCA 4822  
Db  
4476 TTCAAATGGACTTAAATTTGGTTCCACAGCTATTCTGTATAGACAGGAGGTTCCAAA 4535  
Qy  
4823 GACAGGAGCAGATGACGACGACGCTCTCGCGAGTCCGCTACGGAACCTCTCGCAAT 4882  
Db  
4536 AGCA-----ATGTCAATTTACCTTCATCAGCAGGATTTGAATTCGTGGGAAT 4584  
Qy  
4883 GAGATCTTCGATGACAGGTTTGAAGCTCATCAATGAGTACTTTTATGGAGTCAGGATC 4942  
Db  
4585 GAAATTTGATTTAGATTTTAAATTAATAACGAGTATTACTATGTTGTAAGATA 4644  
Qy  
4943 TACCAGGTCAAGACCCAAACCAATGTACATCGGCTGGTGACCAACCCAGTACCA 4998  
Db  
4645 TTTCCCGGCAAGACCTTACACAGCTTTACGTTGGGATGGTTACTACTCAATTTCA 4700

## RESULT 11

US-11-097-143-22561/c  
; Sequence 22561, Application US/11097143  
; Publication No. US2005020858A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE











Db 2398 AGATCTGAGTGGCCCCAAGCATCTCGTTCCGAATTAATGACAAACCTGTTCAAGGAATGTT 2457  
 QY 2587 CACCAACTTCAATCTGGAAGGATGTTCTTCCGGTCACTCAGCTGCTAGTAAAGCTGAG 2646  
 Db 2458 TGAGAAATTTCAACATCGATGGGCTCTTCTTCCAGTCGTAGTTCTCTGAGGAATAAA 2517  
 QY 2647 TTGTGGGTTCTGCTGGGCGGAGAACACAGGTAGACTCCGGTAGCGGGCTCCAGAGGCTA 2706  
 Db 2518 AGTACGCTTCTGCTTGGAGGGCGACATGGAGAAATTCAAAATTTCTTCCCTCCACCTGGGTA 2577  
 QY 2707 CTCCTGGCTGGTGGAGTCTCTCTGCGGAGAGATCTCAGCTGAGGAGCGCTGC----- 2761  
 Db 2578 TGCTCCCTTTTATGAAGCTGTTCTTGCCAAAAGAAAGTTGAAAGTGGAAACACAGCGCGAGA 2637  
 QY 2762 -TTCTACTTCGGCAACCTGTCAAGCGGGCCCTTGGCTGGACCCCGCTAGTAGACAGCA 2820  
 Db 2638 GTACAAAGCAAGAAAGNACTTACACGCGACCTCTGGGGCCCAACAGTTTCCCTGACGCA 2697  
 QY 2821 TACGGCTTTTGTGCGCTTACGCTCTGTTGATATCTTTACAGATTACTCTGCTTACATATGTGA 2880  
 Db 2698 AGCTGCTTACACCCATCCCTGTGGATACAGCCAGATCGTGTGGCTTCCCTCATCTAGA 2757  
 QY 2881 ACAATCAGAGACAAGCTAGCTGAAATATTCAGAAATGTGGGCTATGAATAAGATCGA 2940  
 Db 2758 AAGATAAGAGAAAAACTGGCAGAGAAATATCCATGAACCTCTGGGTTATGAATAAAATTGA 2817  
 QY 2941 AGCAGGCTGGATGTACGGCGCACAGAGAGAACTTGCACAGATCCACCCCTGCTCGT 3000  
 Db 2818 GCTTGGCTGGCAGTATGGTTCGGTTAGAGATGACAAAGAGACAAACCCATGCTGCT 2877  
 QY 3001 GCGCTTTCAGCGCACTCCCGCCGCTGAGAAAGGATACAGATATACAACTTGTCTGTGCAGAC 3060  
 Db 2878 GGAGTTCTCAAGCTGCTGAACAGGAGCGCAATTAACAATGTCTGCTTCAGAC 2937  
 QY 3061 ACTCAAGACTATCTGGCTCTGGGCTACTACTAT---CAGCTAGATAAGCCCTCCAGCAG 3117  
 Db 2938 CCGTGAAGACTTTGTTGGCATTAGGATGTCTGTGGGTATATCAGATGAACATGCTGAAGA 2997  
 QY 3118 CATCCGCAAGTTCGTCTGCCCAATGAACCTTTTCATGCGAGTCCACGGCTACAGCCAGC 3177  
 Db 2998 CAAGGTGAATAAATAAGACTACCCCAAGAAATTAACCAAGCTGACAAAGTGGATACAAAGCTGC 3057  
 QY 3178 ACCACTCGACCTGAGTGTCTCACCTCGACCCAGATGGATGAGTACTAGTAGGCGAGCT 3237  
 Db 3058 CCTATGAACTGAGCTTTATCAACTCACTCCATCGCAAGAGCAATGCTGCAAGATT 3117  
 QY 3238 GGTGAGAACACCCAACTTTGGCCAGGAGAGGATACAGCAGGGATGAGCTTACCG 3297  
 Db 3118 GGCAGAAATGCACATAATGTGTGGCGCGGGATCGAATCCGCGAGGGCTGGACTTATGG 3177  
 QY 3298 ACTTAATGAGGACTCGGACATGATCGATCCCGGACCTGCTGGTCCATACCCGAGGTTGA 3357  
 Db 3178 CATCCAACAGGAGCTAAGAAACAGAAATACTCGCTTGTTCCTCACTCTCTGGA 3237  
 QY 3358 CGATGCCATCAAGAGGCAACAGGAGCACAGCTCGGAGACTGTGAGGACCTGCTGCTGT 3417  
 Db 3238 TGACCGAACAAGAAATCAACAAAGGACAGCCCTCCGAGGCTGTGCGCAGCTGCTGG 3297  
 QY 3418 CTACGGGTATATGCTGGACCCCGCTACTGGGAGCAGCATGAGCACTCTTGTGGAAGC 3477  
 Db 3298 GTACGGCTACACTTGAAGCACC-----AGATCAAGATCATGACGACGAGCCGGAAGT 3351  
 QY 3478 GTCAAAACAGAACAGCGCACTTCAAGACATACCGCGCTGAGAGAACTATGCCCTCAG 3537  
 Db 3352 GTGACGGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCGGAGAGAACCTATGCACTGAA 3411  
 QY 3538 CTCTGGGAGTGCTATCTGAGTTTCAATCTTAACGGCTGAGCTTATGAGGCTCGGCTG 3597  
 Db 3412 GGCAGGACGGTGATATTTGAATTTGAGACGGTCACTGTGGAGACATGAGGGTGTGGT 3471  
 QY 3598 GGTCTACGGCTGATATGGCACCCAGGAATGATGCTCGGACAAAGACAGAACTCTCTGGGCTTT 3657  
 Db 3472 GAGTCGCTCTGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTTGCCCTT 3531

QY 3658 TGATGTTCAATAGAGGAAAAAGTGTACAGCGGTAACTGAGTCTTTTCGCAAGCAATG 3717  
 Db 3532 TGATGCTTCAAGGCCAGCGGTGTCATCAGG---CAATGAACACTATGCGCGCTCTTG 3588  
 QY 3718 GGTCTTGGTGAAGTAGTGGGGTGTCTCTAGATCTCAATTGATAAGACGATAAGTTTCTC 3777  
 Db 3589 GCAAGCAGGCGATGTCTGGGGTGTATGGTTGACATGAACGAACACACCATGATGTTTCA 3648  
 QY 3778 ACTCAACGGTGAAGTTGTTGATGGATGCTCTTGGCGGAGAGACTAGTCTTGTGATGTCCA 3837  
 Db 3649 ACTGAATGGTGAATCTCTTGTGATGATTGAGCTCAGAACTGGCTTTTCAAGCACTTTGA 3708  
 QY 3838 GGGTGACAAA---CTTTGTACCTTGTTCACGCTTGGTGTGCGCCAAAAAGCCAGGTTAAC 3894  
 Db 3709 TGTTCGCGATGGAATTCATACCTGTGTGAGCCCTTGGAGTGGCTCAAGTGGGTAGGATGA 3768  
 QY 3895 ATACGGTCAGAGCTGAACACAGCTGAATATCTTCAACATGTGTGTGTCAGAGGGATA 3954  
 Db 3769 CTTTGGAAAGGATGTGAGCACCCTTGAATAATTTCCATCTGTGGCTTACAAGAGGGCTA 3828  
 QY 3955 TGAACCATTTCTGTCAATATGAAGAGAGAGCTGACTCACTGCTACACCAA-AGACCAGC 4013  
 Db 3829 TGAACCATTTGCGGTTAATAACACAGGATATATACCATGTGGCTGAGCAGAGGGCTCC 3888  
 QY 4014 CCATCTTCGAGAAATACGGATGAGATGATCGACACACAGAAATAGATGTGACAGGATACCA 4073  
 Db 3889 TCAGTTTCTTCAAGTTCCATCAACCATGAACA----TATAGAGGTGACCAAGATAGACG 3944  
 QY 4074 CTGGTTCAAGATACACTCCATGCTCAAGATTTCCCAACACAGTTTG 4121  
 Db 3945 GCACCATAGACAGATTCCCATGTTTAAAGGTCACTCAGAAAGTCTTTTG 3992

RESULT 13

US-10-276-774-552  
 ; Sequence 552, Application US/10276774  
 ; Publication No. US20040053245A1  
 ; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: US/10/276,774  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 09/496,914  
 ; PRIOR FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO 552  
 ; LENGTH: 14302  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-276-774-552

Query Match 16.8%; Score 840.8; DB 8; Length 14302;  
 Best Local Similarity 55.0%; Pred. No. 5e-260;  
 Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;

QY 343 ACAGAGGGTGTGCTGGCTGCGAAGGTCTCGGCAACCGGCACTGCTCTCGGAGAATAT 402  
 Db 217 ACAGAGCTATCTTGGCAGCAGAGGATTGGCAACAGACTTTGTTCTTGGAGTCCAC 276  
 QY 403 TGCCGA---CAAGAACATACCCCTGATCTGTCGAGTGTGTGTTGTCATCGAACAGGC 459  
 Db 277 TTCCAATTCAGAAATGTGCCCCAGACCTCTCCATCTGCACCTTTGTGTCGAGCAGTC 336  
 QY 460 GCTTTCAAGAGCTTTTACAGGATGTGTAACAGCTGCGGGATCTGAAACTG----- 512  
 Db 337 CCTCTCTGTCCGGGGCTGACAGGATGTGCTTAACACCGTGGAGAAATCAGAAAGGCA 396

QY 513 -----GGAAGAAACTTAGGTAAAGGTACCGGTTCTGGTTATCGTAC 555  
Db 397 AGTTGATGTGAAATAATGGAATTCATGATGAAGACTGCTCAAGGTGGTGGTCACTCAAC 456  
QY 556 GCTACTATACCGCAATGTATCTTTTGGGACATCTTTAAACAGTATATGTAACCTGGGCTG 615  
Db 457 ACTCCTCTACCGACATGACATATTTGCTGGCCATCTCTATAGTGGCATGTATCTGTCTG 516  
QY 616 CTTGTCAACATC---ATCATCCAGGATPAAGCTGGCCTTTGACGTGGGTCTGCAACAGCA 672  
Db 517 CTTGTCCACCTCCCGGCTTCAACTGATAAGCTGGCTTTTGAATGTTGGCTTGAAGAGGA 576  
QY 673 CTCCCAAGGTGAAGCTCTGGTGAACCTGCACTCTGCGCAGCAAAACAGAGATCCGAGGG 732  
Db 577 CACCACAGGGAGGGCTTGTGGTGGACCATACACCTGCTCTTAAGCAGCGCATCAGAAGG 636  
QY 733 CGAGAAGGTGCGAGTCCGAGATGACTTGTATCTTAGTCTCCGTGGCCATTGAGAGATACTT 792  
Db 637 AGAAAAAGTACGAGTTGGAGATGACCTCATCTTAGTTAGCGTGTCTCTGAAAGGTACTT 696  
QY 793 GCACACAAAGAAAGAAACGAAGTATCGATAGTGAACCGCTGTTCCACGTGACGCACTG 852  
Db 697 GCACCTGTCTTAGCAACGCGCAGCTTACACGTGATGCGCTTTCCACGACAGACTCTCTG 756  
QY 853 GTCGGTACAGCCCTATGTGTAATCGAGATGAAGTATGTGGGCTATGTGTTGG 912  
Db 757 GAGCGTGGCCCAATCAGCTCAGG-----AAGTGAGCGCAGCCCAAGGGTATCTCATTTG 810  
QY 913 AGGTGATGTGCTCAGGTTCTTCCATGGA---GGTGACGAGTGTCTCACTATACCTAGCAC 969  
Db 811 TGGTGTATGTCTCAGGTTGCTGTGATGACATGACGAGTGTCTCACTGTCCCTCAGG 870  
QY 970 TTGGACAAAGGATGGGGGCAAAATATCGTAGTCTCAAAAGGAGGTTCAAGTATGTCTCA 1029  
Db 871 AGACATCGTGAAGCAGCAGGAGAACTGTTCAATTAAGAGTGGCGTGTGTCTGTCA 930  
QY 1030 AGCCCGTTCTCTATGGCGCTGGAGCTGGCTAGAACCAAGTGGCGGAGGTTTCATTAA 1089  
Db 931 TGCACGTTCCCTTTGGAGACTAGACAGCTAAGAGTTTGGTGGAGTGGAAAGCCACATAAG 990  
QY 1090 CTGTTACCATCTATAGAGTTCCGACATCACTACTGGAAGATATCTTGAGTTAAAGCA 1149  
Db 991 ATGGGGAAGCCATTCGAGTACGCCATGTCAACACAGAAATATCTTGAGTCTCATGGA 1050  
QY 1150 CCAGAAATCAGCTGTATTTAGTTAGCAGAGAGGAACCCACACAGCTTCCCTGTCTCTG 1209  
Db 1051 AGACAAACCTTCTACTCATGGACAAAGAGAAAGCTGATGTAAATCAACAGCATTTAC 1110  
QY 1210 CTTGCGCCAGGAGAAAGGATGATCAGAAGCAAGTGTTAGAAGCAAGGACTTGGAGGTAT 1269  
Db 1111 CTTCCGGTCTTCCAAGGAAAAATTGGATGTAGGGGTGAGA---AAAGAAAGTAGATGGCAT 1167  
QY 1270 AGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCACTGTGACGATTCGGAGACTGG 1329  
Db 1168 GGGAAACTCTGAAAATAAATAACGGTGACTCAGTATGCTATATACAACATGTAGACACAGG 1227  
QY 1330 CTTGTGGCTGTCTTATAAGTCTTAGCAAAACGAAGAAGAAAGCGTGGGTAAAGTAGAGA 1389  
Db 1228 CCTATGGCTTACTTACCAGTCTGTGGAAGTGAATCCGTGAGATGGGATCTATACAAG 1287  
QY 1390 GAAGCAAGCGATTTCTCCAGGAGAGGCAAGATGACAGATGGCCCTCGACCTCTCCAGTTC 1449  
Db 1288 TAAG--GCTATTATGCTATCATGAAGGCCACATGGATGATGGCAATAAGTTTGTTCGAGATC 1344  
QY 1450 ACAGAGGAGAGATCTATGACTGCTCGAGTTATCAGGAAGTGTCTTCGCTGTTCACTAA 1509  
Db 1345 CCAGCATGAAGAAATCACGACAGCCGAGTTATCCGGAGCAGATCTCTCCCTTTTCAATAG 1404  
QY 1510 GTTTATCAATGGCCCTGGAAACTCTTCAAGAGAACCGTGTCTCACTCGATGTTCTTCGCTC 1569  
Db 1405 ATTTATAGGGCCCTTGTATGCTCTCAGCAAGAAAGGAAGGCTTCCACAGTCAATTTGCC 1464  
QY 1570 AGTGAACCTGGCGGAGATGGTGTATGTGTTCAAGATCTCAACCACTACTTCGCAACGCC 1629

Db 1465 TATAGAGTCG-----TAAGCCTAAGTCTGAGGATCTCATTTGGCTACTTCCACCCTCC 1518  
QY 1630 CGATGAGGATATGGAACACGAAGAAAGCAAAACAATTCGCGCCCTCCGCAACCTCA 1689  
Db 1519 AGATGAGCAATTTAGAGCATGAAGACAAACAGACAGACTACGAGCCCTGAAGAAATCGCA 1578  
QY 1690 GGACCTGTTCCAAAGAGGAAGGCATCTGAACCTGATCTCTCGAAGCTATAGACAAGATCAA 1749  
Db 1579 AAATCTCTTCCAGAGAGAGGAATGATCAACCTCGTCTGTGAGTGCAATAGACCGTTTGCA 1638  
QY 1750 CPTGCTCAGCTCCAGCGGGTTCTGCTGATTCCTCGCGGAGACGAATCTGGACAGAG 1809  
Db 1639 CPTCTACAGCAGTGCAGCACATTTGCTGATGTTGCTGGGCGA---GAAGCAGGAGATC 1695  
QY 1810 CTGGGAAATGATATCTGGGATATTTGTATCAAGTTGCTGGCGGCAATAATAAAGGCAACCA 1869  
Db 1696 TTGGAAATCCATTTCTGAATTTCTGTATGAGTTGCTGGCGCTCTAATATTAGAGAAATCG 1755  
QY 1870 CACGAACTGCGCAGTTCGGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGCCTCGG 1929  
Db 1756 TAAAAACTGTGCTCAATTTTCTGGCTC-----CTCGACTGGTTGATCAGGAG 1803  
QY 1930 CTGCGAGCCCTCGGGCGAGGGCACCGGCATGCTGACGTGTGCACTGCACTCTCATCGA 1989  
Db 1804 ATTGGAAGACTGGAAGCTTCTTCAAGCAATCTGGAAGTTTACACGTGTGTTAGTAGA 1863  
QY 1990 CTGCGCTGAAGCGCTCAATATGATGAGGGACGAACACATATAAAGTGAATACTCTCTATT 2049  
Db 1864 AAGTCCAGAAAGCTCTAAATATATTAAAGAAAGGACATATTAAATCTATTATCTCACTTT 1923  
QY 2050 AGAAAGCAAGGAGCGGACCTTAAAGTACTAGATGCTATGTTCACTCTGCGTCGGTAA 2109  
Db 1924 AGACAAACATGGAAGAAATCAAAAGGTTCTGGATGTTCTGTGCTCACTCTGTGTTGCCA 1983  
QY 2110 CGGCGTCCGCTGGCTCGTCAAGAAACAACTCTGCGACTATTGTGCTGCCCGCAAGAA 2169  
Db 1984 CGGGTTGAGTCCGTTCTAAACAGCATCTCATCTGTGACAACTCTCTACAGGAAGAGA 2043  
QY 2170 CTTGTTCTGCTCAAACTCGCTTGTAGATCACTATCTAGTGTCCGTGCGAAGATCTTCGT 2229  
Db 2044 CTTGTTATTGACAGACAGCTCTTGTGAACCATGTCTGAGCATGAGACCAATAATTTTCT 2103  
QY 2230 GGGCGAGTAGAAGGTTGGCAGTGTACCGCAATGTTACTTCCGAGGTGACTATGGACCA 2289  
Db 2104 GGGCGTCAGTGAAGGTTCTGCTCAGTATAAGAAATGGTACTATGAATGTATGTTGGACCA 2163  
QY 2290 CATAGAG---AAGACCACACATATGATGCCACATCTACGCA TAGGATGGGCTAACACTAC 2346  
Db 2164 CACAGACCTTTTGTGACAGCTGAAGCAACTCACTCGAGTGGCTGGGCTTCCACTGA 2223  
QY 2347 TGGTTATGTCCCATACCCGGTGGTGTGAGAAAGTGGGAGGTAAAGCGTGGGAGAGCA 2406  
Db 2224 AGGATATTCTCCCTACCTCGAGGGCGCAAGAGTGGGGTGGAAATGGTGTGGAGATGA 2283  
QY 2407 CTTGTACTCTGACGGGTTGATGGCGCTTACTCTGTGCTCGGCGGAGGAGACCCCGGT 2466  
Db 2284 TCTCTCTCTCTATGGATTTGATGGCCTTCTCTGTGTCAGTTG-----TATTGCTCG 2337  
QY 2467 CAATAGGACTCATCTGAAGAGCCTTATATTAGAAAGGTCACGTGATAGTGTGTGCAATT 2526  
Db 2338 TACTGTAACTCACCAAAACCAAGATCTGTTAAGAACTGATGATGTCTCATCACTGTGTTT 2397  
QY 2527 GGACCTGACGGTACCCCATCATCACTTCACTGTTCAACGAGGTGGGGTGAAGCGGATCCTT 2586  
Db 2398 AGATCTGAGTGGCCCAAGCATCTCGTTCCGAAATTTAATGGACAACTGTCTCAAGGAATGTT 2457  
QY 2587 CACCAACTTCAATCTGGAAGCATGTTCTTCCCGCTCATCAGCTGCTCTAGTAGAGCTGAG 2646  
Db 2458 TGAGAAATTTCAACATCATGATGGCCTCTTCTTCCAGTCTGTTAGTTTCTCTGAGGAATAA 2517  
QY 2647 TTGTGCGTTCTGCTGGCGGAGAACCGGTAGACTCCGGTAGCTCCGGTCCAGAGGCTA 2706

2518 AGTACGCTTTCTGCTGGAGGCGACATGAGAAATTTCAAATTTCTTCCACCTGGGTA 2577  
QY  
2707 CTCCTCCGCTGGTGGAGTCTCTCTCGCGCAGCAGATCCTCAGCTGGAGCGGTGC----- 2761  
Db  
2578 TGTCTCTTGTATGAAAGCTTGTCTGCGCAAAAGAAAGTTGAAAGTGAACACAGCGGAGA 2637  
QY  
2762 -TTCTACTTTCGGAACCTGTCCAAGCGGCGCTTGGCTGGACCCCGCTAGTACAGAGCA 2820  
Db  
2638 GTACAGCAAGAAGAACTTACACACGCGACCTGTGGGCCCCACACAGATTTCCTGACGCA 2697  
QY  
2821 TAGGGCTTTTGGCTTACCGCTGTGTGATCTTTACAGATTAATCTGCTCCATATATGGA 2880  
Db  
2698 AGCTGCTTTTACACCCATCCCTGTGGATACCAAGCCAGATCGTGTGCTCTCCATCTAGA 2757  
QY  
2881 ACAATACAGAGCAAGCTAGCTGAAATATTCACGAAATGTGGCTATGAAATAAGATCGA 2940  
Db  
2758 AAGATTAAGAGAAAACCTGGCAGAGATATTCATGAACTCTGGTTATGAAATAAATTTGA 2817  
QY  
2941 AGCAGGCTGGATGTACGGCGACCCAGAGAGAAGACTTTGCAAAAGATCCACCCCTGCTGT 3000  
Db  
2818 GCTTGGCTGCGAGTATGGTTCGGTTAGAGATGACAAAGAGACAAACCCATGCTGTGT 2877  
QY  
3001 GCGCTTCGAGCGACTCCCGCCCGCTGAGAAAACGATAGATATACAACTTGTGTGAGAC 3060  
Db  
2878 GGAGTTCTCAAGCTGCTGAAACAGGAGCGCAATTAACAATTTACAAATGTGCTTTGAGAC 2937  
QY  
3061 ACTCAGAGCTATCCTGGCTCTGGCTACTACAT---CAGCTTAGATAAGCCTCCAGCAG 3117  
Db  
2938 CTTGAAGACTTTTGTGGCATTTAGGATGTCTATGGGTATATCAGATGAACATGCTGAAGA 2997  
QY  
3118 CATCCGCAAGCTTGTCTGCCCAATGAACTTTTCATGCAGTCCAAAGCTTACAAAGCCAGC 3177  
Db  
2998 CAAGGTGAAAATAAGAGCTACCAAGATTTACCAAGCTGACAAAGTGGATACAGGCTGC 3057  
QY  
3178 ACCACTGCACTGAGTGTGTACCTCTGACACCCAAAGATGATGATGATGATGATGATGAT 3237  
Db  
3058 CCTATGGACCTGAGCTTTATCAAACTCAACCCATCCGCAAGCAATGGTGACAAAGTT 3117  
QY  
3238 GCGTGAGAACACCCACAACTTTGGCCGAGGAGAGATACAGCAGGATGACTTACCG 3297  
Db  
3118 GGCAGAAATGACATAATATGTGTGGCGCGGATCGAATCCGCGAGGCTGCGCAGCTGATGG 3177  
QY  
3298 ACTTAATGAGACTCGGACATGCTATCCCGCACCTGTGCGCATACCCGCAAGCTTGA 3357  
Db  
3178 CATCCAGAGAGCTTAAAGACAGAGAAATCTCGCCTTGTTCCTACACTCTCTGA 3237  
QY  
3358 CGATGCCATCAAGAGGCAACAGGACACAGCCTCGGAGACTGTGAGAACCTGTGTGT 3417  
Db  
3238 TGACCGAAACCAAGAAATCCAAACAGGACAGCCTCCGCGAGGCTGTCGCGACGCTGCTGG 3297  
QY  
3418 CTACGGGTATGCTGGACCCGCTACTGGGGAGCAGCATGAGCACTCTTGTGGAAGC 3477  
Db  
3298 GTACGGCTCAACTTGGAAAGCACC-----AGATCAAGATCATGCGCAGAGCCGAAGT 3351  
QY  
3478 GTCAAAACAGAAAGCCGACTTCAGAACATACCGGCTGAGAGAAATATGCGGCTCAG 3537  
Db  
3352 GTGACGGGCAACCGGGAAGGTTCCGAATCTTCCGTGCGAGAGAACCTATGCAAGTGA 3411  
QY  
3538 CTCTGGGAAGTGTACTCTGAGTTTGAATCTTAACGGCTGGACCTATGAGGCTGGCTG 3597  
Db  
3412 GCGCGGACGGTGTATTTGAAATTTGAGACGGTCACTGTGGAGACATGAGGGTGTGGTTG 3471  
QY  
3598 GCGTCAAGCTGATATGGCACCAGGAATGATGCTCGGACAGAGCAATCTCTGGGCTTT 3657  
Db  
3472 GAGTCGCTCTGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTCCTTTGCCCTT 3531  
QY  
3658 TGATGTTCAATGAGGAAAAAGTGTACAGCGGTAAACCTGAGTCTTTTCGGCAAGCAATG 3717  
Db  
3532 TGATGCTTCAAGGCCAGCGGTGGCATCAGGG---CAATGAACATATGGGGCTCTTTG 3588  
QY  
3718 GCGTGTGTGAGTGTGGGGTGTTCCTAGATCTCATTTGATTAAGACGATAGTTTCTC 3777  
Db  
3589 GCAAGCAGGCGATGCTGCGGGTGTATGGTTGACATGAACGACACACCATGATGTTTCA 3648

QY 3778 ACTCAACGGTGTGATGTTGTTGATGGATGCTCTTTGGCGGAGAGACTACGTTTGTGATGTCCA 3837  
Db  
3649 ACTGAATGGTGAATCCCTTCTTGATGATTAGGCTCAGAACTGGCTTTTCAAGGACTTTGA 3708  
QY 3838 GGGTGACAA---CTTTGTACCTGCTTGACAGCTTGGTGTGCGCCAAAAGCCAGGTTAAC 3894  
Db 3709 TGTGGCGATGGATTCATACCTGTGTAGCCCTGGAGTGGCTCAAGTGGGTAGGATGAA 3768  
QY 3895 ATACGGTTCAGGACGTGAACACACGCTCAAAATACCTTCAACAATGTGCTTGCAGAGGGATA 3954  
Db 3769 CTTTGGAAAGGATGTCAGACCTTGAATATTTTCAACATCTGTGCTTACAAGAGGGCTA 3828  
QY 3955 TGAAACCATTTCTGTGTCAATATATGAAGAGAGACGTGACTCACTGTTACACCAA-AGACCAGC 4013  
Db 3829 TGAACCATTTTGGCGTTAATACAAACAGGATATTACCATGTGGCTGAGCAGAGGGCTTC 3888  
QY 4014 CGATCTTCGAGATACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4073  
Db 3889 TCAGTTTCTTCAAGTTTCCATCAACCATGAACA----TATAGAGGTGACCAAGATAGACG 3944  
QY 4074 CTGGTTTCAGATACACCTCCATGCTCAAGATTTTCCCAACAACACGTTTG 4121  
Db 3945 GCACCATAGACAGTTCCCATGTTTAAAGTCACTCAGAAAGTCTTTTG 3992

RESULT 14

US-10-887-553A-490  
; Sequence 490, Application US/10887553A  
; Publication No. US20050085436A1  
; GENERAL INFORMATION:  
; APPLICANT: Garza, Dan  
; APPLICANT: Li, Hao  
; TITLE OF INVENTION: Method to treat conditions associated  
; TITLE OF INVENTION: with insulin signalling dysregulation  
; FILE REFERENCE: 4-33262  
; CURRENT APPLICATION NUMBER: US/10/887,553A  
; PRIOR APPLICATION NUMBER: 2004-07-08  
; PRIOR FILING DATE: 2003-08-07  
; NUMBER OF SEQ ID NOS: 1208  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 490  
; LENGTH: 15731  
; TYPE: DNA  
; ORGANISM: human  
US-10-887-553A-490

Query Match 16.8%; Score 840.8; DB 10; Length 15731;  
Best Local Similarity 55.0%; Pred. No. 5.3e-260;  
Matches 2105; Conservative 0; Mismatches 1622; Indels 101; Gaps 19;

QY 343 AGAGAGGGTGTGCTGGCTGCGGAGGTTCTCGGCAACCGGCACTGCTTCTCGAGATAT 402  
Db 217 ACAGAAAGCTATGCTTGGCAGCAGAAAGGATTTGCGCAACAGACTTTGTTCTTGGAGTCCAC 276  
QY 403 TGCCGA---CAAGAACATACCGCTGATCTGTCGAGTGTGTTGTTCATCGAACAGGC 459  
Db 277 TTCCAATCCAAAGATGTGCCCCCAGACCTCTCCATCTGCACTTGTGCTGGAGCAGTC 336  
QY 460 GCTTTTCAGTAAGAGCTTTTACAGGAGTTGGTAAACAGTGTGGGATCTGAAACTG----- 512  
Db 337 CCTCTCTGTCCGGCGCTGCAGGATGCTGGCTAACACCGTGGAGAAATCAGAGGGCA 396  
QY 513 -----GGAAAGAAAACTTAGGTAAAGTACCGGTTCTGGTTATCGTAC 555  
Db 397 AGTTGATGTGGAATAATGGAATTCATGATGAAGACTGCTCAAGGTGGTGGTCAAC 456  
QY 556 GCTACTATACGCAATGCTATTCTTTTGGGACATCTTAACAGTGTATGTACTCTGGCTG 615  
Db 457 ACTCCTCTACGACATGCCATATGCTGGCCATTCCTATAGTGGCATGTATCTGTGCTG 516  
QY 616 CCTGTCAACATC---ATCATCCAGGATAAGCTGGCCTTTTGAGGTGGGTCTGCAACAGCA 672

[illegible]

Db	1579	AAATCTCTTCCAGGAAGGGAATGATCAACCTCGTGTGCTTGTAGTGCAATAGACGCTTTGCA	1636
Qy	1750	CGTGGTCAACGCTCCAGGGGTTCTCGGCTGATATTCCTGGCGGGAGAGCAAAATCTGGACAGAG	1809
Db	1639	CGTCTACAGCAGTCAGACACATTTGCTGATGTTGCTGGSCGA--GAAGCAGGAGATC	1695
Qy	1810	CTGGAAATGATATCTGGATATTTGTATCATAGTTGCTGGCGGCAATATATAAAGGCAACCA	1869
Db	1696	TTGGAAATCCAATTCGTAATTTCTGTATGATGTTGCTGGCGGCTCTAATTAAGAGGAATCG	1755
Qy	1870	CACGAATCGCGCGNGTTCCGGAACTCGAACCGGTCAACTGGCTGTCTTCGCGCCTCGG	1929
Db	1756	TAAAAACTGTGCTCAATTTTCTGGCTC-----CCTCGACTGGTTGATCAGCAG	1803
Qy	1930	CTCGACGGCCTCGGCGGAGGCAACCGGCATGCTCGACGTCTGCATCGCATCTCATTCGA	1989
Db	1804	ATTGGAAGACTGGAAGCTTCTTCAGGCATTTCTGGAAGTTTACACTGTGTTTTAGTAGA	1863
Qy	1990	CTCGCCTGAAGCGCTCAATATGATGAGGAGCGAACACATATAAAGTGATTAATCTCTCTATT	2049
Db	1864	AAGTCCAGAAAGCTCTAAATATTAATAAGAGACATATTAATAATCTATTATCTCACTTTT	1923
Qy	2050	AGAAAAGCAGGACGCGACCTTAAGTACTAGATGTCTATGTTTCACTCTCGCTCGGTAA	2109
Db	1924	AGCAAACTGGAAGAAATCACAAAGTTCTGGAATGTTCTGTGTCACTCTGTGTTGCCA	1983
Qy	2110	CGGCGTCGCGTGGCTCGTCAAGAACAACTCTCGACTATTGTCGCCCGGCAAGAA	2169
Db	1984	CGGGTTGCAGTCCGTTCTAACCAAGCATCTCATCTGTGACAACTCTCTACCAGNAGAGA	2043
Qy	2170	CTGTGCTGCAAACTCGCGCTTGTAGATCAGTATCTAGTGTCCGTCCGGAACATCTTCGT	2229
Db	2044	CTTGTTATTGCAGACACGTCTTGTGAACCATGTCAAGCATGAGACCCCAATATTTTTCT	2103
Qy	2230	GGGCGGAGTAGAGGGTTCGCGAGTGTTACCGCAAAATGCTACTTCGAGGTGACTATGACCA	2289
Db	2104	GGGCGTCAGTGAAGGTTCTGCTCAGTATAAGNAATGGTACTATGAATTGATGGTGGACCA	2163
Qy	2290	CATAGAG---AAGACCACATATGATGCCACATCTACGCATAGGATGGGCTAAACACTAC	2346
Db	2164	CACAGAGCCCTTGTGACGCTGAGCAATCACCTCGAGTGGGCTGGGCTTCCACTGA	2223
Qy	2347	TGGTTATGTCCCATACC CGGGTGGTGTGAGAAAGTGGGAGGTAAACGGCTGGGAGACGA	2406
Db	2224	AGGATATTCTCCCTACCTCGAGGGGCGAAGAGTGGGCTGGAATGGTGTGGAGATGA	2283
Qy	2407	CTGTACTCGTAGCGGTTGATGGCGCTACTCTGTCCGGCGGAGGAAGACCCCGGT	2466
Db	2284	TCTCTTCTCTATGGAATGATGGCCTTCACTCTGTCTAGGTTG-----TATGTCTCG	2337
Qy	2467	CAATAGACTCATGCTCAAGAGCCTTATATTAGAAAGGTGACGTGATAGGTTGTGCATT	2526
Db	2338	TACTGTAGCTCACCAACCAACATCTGTTAAGAACTGATGATGATCATCAGTTGCTGTTT	2397
Qy	2527	GGACCTGACGGTACCCATCATCACTTATGTTCAACGGAGTGGGGTGAAGGATCCCTT	2586
Db	2398	AGATCTGAGTGCCCCAAGCATCTCGTTCCGAAATTAATGGACAACCTGTTCAAGGAATGTT	2457
Qy	2587	CACCAACTTCAATCTGAAGAGCATGTTCTTCCGGTCACTCAGCTGTCTTAGTAAGCTGAG	2646
Db	2458	TGAAATTTCAACATCAATGGCCTCTTCTTCCAGTGGTTAGTTTCTCTCGAGGAATAAA	2517
Qy	2647	TTGTTCGGTTCTGTCTGGGCGGAGAACGCTAGACTCCGGTACCGGCTCCAGAAAGCTA	2706
Db	2518	AGTACGCTTTCTGTCTGGAGGGGACATGAGGAATTCAAATTTCTTCTTCCCTCCACTGGGTA	2577
Qy	2707	CTCCCCGCTGGTGGAGTCTCTCTCTGCCGAGCAGATCCTCAGCCTGGAGCCGTGC-----	2761
Db	2578	TGCTCTCTTGTATGAGCTGTTCTGCCAAAGAAAAGTTGAAAGTGGAACACAGCCGAGA	2637
Qy	2762	-TTCTACTTCGGCAACTGTCTCAAGCGGGGCTTGGCTGGACCCCGCTAGTACAGGACGA	2820
Db	2638	GTACAGCAAGAAAGAACTTACACACGCGACCTGCTGGGCCCCACAGTTCCTCTGACGCA	2697



QY 2821 TACGGCTTTTGTGCTTACGCTTGTGATCTTTACAGATTTACTCTGCTTACATATGTGGA 2880  
DB 2698 AGCTGCTTACACCCATCCCTGTGGATACACGACGATCGTGTGCTCTCATCTAGA 2757  
QY 2881 ACAATACAGAGACAGCTAGCTGAAATATTCAGAAATGTGGGCTATGAATAAGATCGA 2940  
DB 2758 AAGAATAAGAGAAAACTGGCAGAGAAATATCCATGAATCTCTGGTTATGAATAAAATGGA 2817  
QY 2941 AGCAGCTGGATGTACGGGACACAGAGAGAGACTTGCACAAGATCCACCCCTGCTCGT 3006  
DB 2818 GCTTGGCTGGAGTATGTGTCGGTTAGAGATGACAAACAGAGACACCCATGCTGTGT 2877  
QY 3001 GCCCTTCGAGCGACTCCCGCTGAGAAACGATACGATATACAACTTGTGTGTCAGAC 3060  
DB 2878 GGAGTTCTCAAGCTGCCGTGAACGAGGCGCAATTACAATTACAATGTCTGCTTGAGAC 2937  
QY 3061 ACTCAAGACTATCTGGCTCTGGGTACTACAT---CAGCTTAGATAAGCCTCCAGCAG 3117  
DB 2938 CTTGAAGACTTTGTTGGCATTAGGATGTCTATGTGGGTATATCAGATGAACATGCTGAAGA 2997  
QY 3118 CATCCGACAGTCTGCTGCCCAATGAACCTTTTCATGCAGTCCACGGCTACAAGCCAGC 3177  
DB 2998 CAAGGTGAAAAAATGAAGCTACCCAGAAATTACCAGCTGACAAAGTGGATACAAGCCTGC 3057  
QY 3178 ACCACTCGACCTGAGTGTCTCACCTGTGACCCAGATGGATGAGCTAGTAGGCCAGCT 3237  
DB 3058 CCTATGGACCTGAGCTTTATCAACTCACCCATCGCAAGAGCAATGTGTGCAAGTT 3117  
QY 3238 GGCTGAGAACACCCCAACCTTTGGCCAGAGGAGAGATACAGCAGGGATGGAATTACGG 3297  
DB 3118 GCGAGAAATGACATATGTGTGGCGGGGATCGAATCCGCGAGGCTGGAATTATGG 3177  
QY 3298 ACTTAATAGAGACTGCGACATGATGCCCGACCTGTGGTGCATACCCGAAGTTGA 3357  
DB 3178 CATCAACAGGACGTAAGAAACAGAGAAATCTCGCTTGTTCCTACACTCCTCTGGA 3237  
QY 3358 CGATGCCATCAAGAGGCCCAACAGGACACAGCTCGGAGACTGTGAGGACCTCGTGTGT 3417  
DB 3238 TGACCGAATCAAGAAATCAACAAAGGACAGCTTCGCGAGGCTGTGCGACGCTGCTGGG 3297  
QY 3418 CTACGGGTATATCTGCAACCGCTACTGGGAGCAGCATGAAGCACTCTTGTGGAAGC 3477  
DB 3298 GTACGCTACACTTGGAGCACC-----AGATCAAGATCATGACGACGAGCCGAAT 3351  
QY 3478 GTCAAAACAGAACAGCGACTTTCAGAAACATACCGCGCTGAGAGAACTATGCGCTCAG 3537  
DB 3352 GTGACGCGCACCGGGGAAAGGTTCCGAATCTTCGCTGCGAGAGACCTATGCAGTGAA 3411  
QY 3538 CTCTGGGAAGTGTACTTTCAGTTTTCAGATCTTAACGGCTGGACCTATGAGGCTGGCTG 3597  
DB 3412 GCGCGACGCTGTATTTGAATTTGAGACGCTCACTGTGGAGACATGAGGCTGGTTG 3471  
QY 3598 GGTCTACGCTGATATGGCACCGAATGATGTGCGACAGAGACGAACTCTCTGGGCTTT 3657  
DB 3472 GAGTCTCTGTTGTCAACCGAATCAGAGCTTGGCTCAGATGAACGCTGCTTGGCTT 3531  
QY 3658 TGAATGTTCAATAGAGAAAAAGTGTACGCGGTAACTAGTGTCTTTCGCGAAGCAATG 3717  
DB 3532 TGATGCTTCAAGGCCACCGGTGGCATCAGG---CAATGAACACTATGCGGCTCTTTG 3588  
QY 3718 GGTGTTGGTACGATAGTGGGGTGTTCCTAGATCTCATTGATGAACAGATAGTTTCTC 3777  
DB 3589 GCAAGCAGGCGATGTCTGGGGTGTATGTTGATGAATGAACAGAAACACACCATGATGTTCA 3648  
QY 3778 ACTCAACGCTGAGTGTGTGATGATGCTCTTGGCGGAGAGACTACGCTTTGCTCATCTCA 3837  
DB 3649 ACTGAATGGTGAATCTCTTGTGATGATCAGGCTCAGAACTGGCTTTCAAGGACTTTGA 3708  
QY 3838 GGGTGAACA---CTTTGTACTCTGCAAGCTTGGTGTGCGGCGCAAAAAAGCCAGGTTAAC 3894  
DB 3709 TGTGGGATGGATTCATACCTGTGTGACCTTGGAGTGGCTCAAGTGGGTAGATGAA 3768

QY 3895 ATACGCTCAGACGCTGAACACGCTGAATACTTTCACACATGTGGTCTGCAGAGGGATA 3954  
DB 3769 CTTTGGAAAGGATGTGCAGCACCCTTGAATATTTCCACCATCTGTGGCTTACAAAGGGCTA 3828  
QY 3955 TGAACCATTCCTGTGTCATATGAAGAGAGAGCTGACTCACTGGTACACAA-AGACCAGC 4013  
DB 3829 TGAACCATTCCTGCGTTAATACAAACAGGGATTTACCATGTGGCTGAGCAAGAGCTTCC 3888  
QY 4014 CGATCTTCGAGAAATACCGATGAGATGATCGACACAGAAATAGATGTGACCCAGGATACCAG 4073  
DB 3889 TCAGTTTCTTCAAGTTCCATCAACCATGAACA---TATAGAGGTGACCAAGATAGACG 3944  
QY 4074 CTGGTTTCAAGTACACCTCCATGCTCAAGATTTCCCAACACAGTTTG 4121  
DB 3945 GCACCATAGACAGTTCCCATGTTTAAAGGTCACTCAGAAAGTCTTTTG 3992

RESULT 15  
US-10-276-774-500  
; Sequence 500, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 500  
; LENGTH: 15359  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-500

Query Match 16.6%; Score 831.4; DB 8; Length 15359;  
Best Local Similarity 54.8%; Pred. No. 5.9e-257;  
Matches 2083; Conservative 0; Mismatches 1611; Indels 105; Gaps 18;

QY 265 GGGGGGACAGCAGCAGAGAGAGAGG-----TGTGCTTGGCTGCCGAAAGGCT 372  
DB 133 GGGTCAACGAGAGGCGAAGCAGAGTCCAGTCTCGGACGAGATGTGCCCGCGAGGCTT 252  
QY 325 GTGCTGTCACAGCAGCAGGAGAGAGG-----TGTGCTTGGCTGCCGAAAGGCT 372  
DB 193 GCAGTGCAGCGCTACCGTCTCAAGAGCAGCTCAAGCTCTGCTGGCGCGAGGCTT 252  
QY 373 CGGCAACCGGCACTGCTTCCGAGAAATATGCCGACA---AGAACATACCCGCTGATCT 429  
DB 253 CGGCAACCGCTGTGCTTCCGAGCCCACTAGCAACGCGAGAAATGTGCCCGCGATCT 312  
QY 430 GTGCGAGTGTGTTTGTTCATCGAACAGCGCTTTTCAGTAAGAGCTTTTACAGAGTTGCT 489  
DB 313 GCGCATCTGTGCTTGTGCTTCCGAGAGCTTCCCTGTCTGTGCGAGCCCTCAGAGATGCT 372  
QY 490 AACAGCTGGCGATCTGAAACTGGGAAAGAAAACTTAGTAAAGGTACCGGTTTCTGGTTA 549  
DB 373 -----GGCTAACCGTGGAGGCTGGAGTCCAGGGCGGGGACA 420  
QY 550 TCGTACGCTATATACGGCAATGCTATTTCTTTTGGACATCTTAACAGTGAATGTACCT 609  
DB 421 CAGGACGCTCTGTATGGCCATGCCATCTCTGCTCGGATGCACACAGCCGATGTATCT 480  
QY 610 GCGTGCCTGTCAACATCATCTCCAG---CATAGCTGGCTTTGACGTGGTCTGCA 666  
DB 481 GAGCTGCTTCAACACCTCCGCTCCATGACTGACAAAGCTGGCTTCGATGTGGGACTGCA 540  
QY 667 ACAGCACTCCCAAGGTGAAGCCTGCTGTGGAGCCCTGTCATCTGCCAGCAACAGAGATC 726





Qy 3946 GGAGGGATATGAACCATTTCTGTCAATATATGAAGAGAGCGTGACTCACTGGTACACCAA 4005  
Db 3787 GGAAGGCTTCGAGCCATTTGCCATCAACATGACAGGCCACCTGCTTTCAGCAA 3846  
Qy 4006 AGACCAGCCGATCTTCGAG 4024  
Db 3847 AGGCTGCCCCAGTTTGAG 3865

Search completed: October 10, 2006, 16:48:33  
Job time : 3842 secs

Qy 2872 ATATGTGGAACAAATCAGAGACAAGCTAGCTGAAATATTTACGAAATGTGGCTATGAA 2931  
Db 2722 CCATCTGGAGCGCATTCGGGAGAAGCTGGGGAGAACATCCACAGGCTCTGGCGCTAAC 2781  
Qy 2932 TAAAGATCGAAGCAGGCTGTGATGTCGGGACACAGAGAGAGACTTTGGCAACAGATCCACCC 2991  
Db 2782 CGGCATCGAGCAGGCTGGACCTACGGCCCGTTCCGGATGACAAACAGAGGCTGCACCC 2841  
Qy 2992 CTGCTCTGGCCCTTCGAGCGACTCCGCCCTGAGAAACGATACGATATACAACTTGC 3051  
Db 2842 GTGTCTTGTGGACTTCCACAGCCTTCAGAGCCTGAGAGAACTAACCTCGCATGTC 2901  
Qy 3052 TGTGACAGACACTCAAGACTATCTGGCTCTGGGCTACTACATCAGCTT---AGATAAGCC 3108  
Db 2902 TGGGGAGACGCTCAAGACTCTGCTGGCTCTGGCTGCCACGTTGGGATGGAGAA 2961  
Qy 3109 TCCAGACGCATCCGGAACGTTGCTGCTGCCCAATGAACCTTTTCATGTCAGTCCAAACGGCTA 3168  
Db 2962 GCGGGAGGACAACTGAAGAAGACAAAACTCCCCAAAGACGTATATGATGAGCAATGGGTA 3021  
Qy 3169 CAAGCCAGCACCCTCGACTGAGTCTGTACCTCTGACCTGACACCAAGATGGATGACTAGT 3228  
Db 3022 CAAGCCGGCTCCGCTGGACTGAGCCACGTCGGGCTGACGCCGGCGCAGACAACTGGT 3081  
Qy 3229 AGGCCAGCTGGCTGAGAACACCAACCTTTTGGGCCAGGGAGAGGATACAGCAGGGATG 3288  
Db 3082 GACCGCTTGGCAGAAATGGGCAACACGTGTGGGCCCGAGACCCTGGTGGGCCAGGGCTG 3141  
Qy 3289 GACTTACGGACTTAATGAGGACTCGGACATGATCGATCCCGCACCTGGTGCCTATGCC 3348  
Db 3142 GAGCTACAGCGAGTCAGGACATCCACGCGCGCGAAACCTCTGGCTGGTGCCTACCG 3201  
Qy 3349 GAAGGTTGACGATGCCATCAAGAGGCCCAACAGGGACACAGGCTCGGAGACTGTGAGGAC 3408  
Db 3202 CCTGTGGATGAAGCCACCAAGCGCAGCAACCGGGACAGCCCTTGCAGGCCGTGGCGAC 3261  
Qy 3409 CTGTCTGGTCTACGGGTATATGCTGGACCCGCTACTGGGGAGCAGCATGAAGCACTCTT 3468  
Db 3262 CTTCTGGCTACGGCTACACATCGAGCTCTGTACAGGAGCCCGTCA----- 3312  
Qy 3469 GTTGAAGCGCTCAAAACAGAGCAAGCCGACTTCAGAAATACCGCGCTGAGAAAGACTA 3528  
Db 3313 ---GGTGGAGAACAGTCTCTGTTGTGACCGGTGGGCACTTCCGGGCAGAGAAATCCTA 3369  
Qy 3529 TGGCGTACGCTCTGGGAAGTGTACTTCGAGTTTGAGATCCCTAACGGCTGGACCTATGAG 3588  
Db 3370 TACAGTGCAGAGCGCGCTGGTACTTCGAGTTTGAAGCAGTCAACACAGGGGAGATGCG 3429  
Qy 3589 GGTCCGCTGGGCTCACGCTGATATGGCACCCAGGAATGATGCTCGGACAGACGAGAACTC 3648  
Db 3430 CGTGGGCTGGGGAGCCCGAGCTGAGGCTGATGTAGAGCTGGGAGCTGACGAGTGGC 3489  
Qy 3649 CTGGGCTTTTGTGTTTCAATGAGGAAAAAGTGTACAGCGGTAACTACCTAGTCTTTCCG 3708  
Db 3490 CTATGTTCTCAATGGGCAACCGCGCCAGCGCTGGCACCTTGGG---CAGTGAACCAATTTGG 3546  
Qy 3709 CAAGCAATGGGCTGTTGGTGAACGTAAGTGGGGGTGTTCTTAGATCTCAATTTGATAAGACGAT 3768  
Db 3547 GCGCCCTGGCAGCCGGGGGATGTCGTTGGCTGTATGATCGACCTCAACAGAGAAACACCAT 3606  
Qy 3769 AGTTTCTCACTCAACGCTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGC 3828  
Db 3607 TATCTTACCCCTCAATGGGGAGGTCTCATGCTGACTCAGGCTCCGAAACAGCCTTCGG 3666  
Qy 3829 TGATGTCAG---GGTGACAACTTTCTACTGCTGTCAGCGCTGGTGTGGCCAAAAAGC 3885  
Db 3667 GGAGATTGAGATTGGGGAACGGCTTCTGCCCCGCTCGAGCTTGGGACTGGCCAGGTGGG 3726  
Qy 3886 CAGGTTTAACTACGGTCAAGACCGTGAACACGCTGAAATATCTTCAACATGTGGTCTGCA 3945  
Db 3727 TCATCTGAACTTGGGCCAGGACGTGAGCTCTCTGAGGTTCTTTGCCATCTGTGGCCTCCA 3786

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Query Match	16.4%;	Score 821.4;	DB 8;	Length 15563;
Best Local Similarity	54.8%;	Pred. NO. 2.8e-243;		
Matches 2082;	Conservative	0;	Mismatches 1531;	Indels 102; Gaps 18;
QY	346	GAGGGTGCTGGCTGCCGAAAGGTCGCGCAACGGCACTGCTTCCTGAGAAATATGC	405	
Db	172	GAAATTCCTGCTGGCAGCGAGGAACTTGGGAATCGCGTGTGCTTCCTTGGAAACCCATCTC	231	
QY	406	CGA---CAAGAAACATACCGCCTGATCTGTGCGAGTGTGTTTTGTCTATCGAACAGGCGCT	462	

Db 222 AGAAGCCAAAGTACATCTCTCCAGATCTCTGGTCTGCAATTTTGTCTGGAAAGTCCCT 291  
Qy 463 TTCAAGAGAGCTTTTACAGGAGTTGGTAAACAGCTGCGGATCTGAAACTGGGAAGAAA 522  
Db 292 ATCTGTACAGCCCTGCAGGAATGCTTGGCCAAACACAGG-----TGAATATGGCG 342  
Qy 523 CTTAGTAAAGGTACCGGTTCTGGTTATCGTACGCTACTATACGGCAATGCTATCTTTT 582  
Db 343 CGAAGGGCAGCACAAAGAGGTGGCCACAGACCCCTGTTATACGGCCATGCAAGTTCTCCT 402  
Qy 593 GCGACATCTTAACAGTATATGTAACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 639  
Db 403 GAGGACATCTTTACGGGAAATGTAATCAACATGCTTGACTACATCAAGATCCCAGACGA 462  
Qy 640 TAAGTGGCCTTTGACGTGGGTCTGCAACAGCACTCCCAAGGTGAAGCTGCTGCTGGAC 699  
Db 463 CAACTTGGCTTTGATGATGATGCTACGGGAATGCTCCACAGAGAAAGCTGTTGGTGAC 522  
Qy 700 CCGTCACTCTGCGACCAACAGAGATCCGAGGGCGAGAGGTGGAGTGGAGATGACTT 759  
Db 523 TATACATCTGCTTCCAAACAGAGTCCGAAAGGAGAAAGTTGCAATTTGGCGATGACCT 582  
Qy 760 GATTTAGTCTCCGTGGCCATGAGAGATCTTGCACACCAAGAGAGAAAGTATC 819  
Db 593 CATCTCGTCAAGGTGCTCTGAAAGATACCTTCACTCTCAATCAAAATGGTAACAT 642  
Qy 820 GATAGTGAACCGCTCGTTCCAGCTGACGCACTGGTGGGTACAGCCCTATGCTACTGGTAT 879  
Db 643 ACAAGTGAATGCTCTTTATGCAACACTCTGGAATGTACATCC-----TACGTGCTC 696  
Qy 880 ATCGAGGATGAAGTATGTGGGCTATGTGTTGGAGGTGATGTCTCAGGTTCTTCCATGG 939  
Db 697 AGGAAGTAGCATCGAAGAGGATACCTACTTGGTGGCATGTAGTACGCTCTTTTCCATGG 756  
Qy 940 AGGTACAGATGTCTCACTATACCTAGCATTGGACAAAGATGGGGGCAAAATATCGT 999  
Db 757 TCATGATGAATTTTGAGCATACCACTACAGACCAGAAATGATCCCAAGCAGGAGAT 816  
Qy 1000 AGTCTACAAAGGAGGTTCAGTATGTCTCAAGCCGTTCTCTATGGCGCTGGAGCTGGC 1059  
Db 817 ATTCTACGAAGCTGGGGAGCTGGGACTCGAGCCAGGTCTCTTTGGAGATGGAACCCCT 876  
Qy 1060 TAGAACCAAGTGGCGGAGGTTTCATTAACTGGTACCACTCTATGAGATTCGGCAAT 1119  
Db 877 TCGGATAAGCTGAGTGGCAGTAACATCAGATGGGGCCAGGCTTTCCGACTCCGGCATCT 936  
Qy 1120 CACTACTGGAAGATATCTTGGAGTTAACGACCAGATGAGCTGATTTAGTTAGCAGAGA 1179  
Db 937 CACCACAGGCCACTACCTGGCCTTGACAGAAAGCAAGGCCCTTATCTGCAAGACCGGC 996  
Qy 1180 GGAACCCCAACAGCTTCTGTGCTCTGCTCGCCGAGGAGAGAGGATGATCAGAAGCA 1239  
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Db 1057 ATTAGACTCCAGTCAACAGGAGACATAGAAGGCATGGAGTTCCAGAAATCAAGTATGG 1116  
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Db 1117 AGATTTCTGTCTGTTGTGCAGCATATAGCCAGTGGTCTGTGGGTGACCTACAAAGCACA 1176  
Qy 1354 CGAAACGGAAGAAAGGCGTGGTAAAGTAGAAGAGAAAGCAAGCGATTCTCCAGGAGA 1413  
Db 1177 AGACGGCAAACTTCCCGCTGGGACCTCTAAAGAAAG---GTCACTATCCATCAGA 1233  
Qy 1414 AGGCAAGATGGAAGTATGGCTCGACCTCTCCAGGTACAGGAGGAGAAATCTATGACTGC 1473  
Db 1234 AGGCCACATGGATGATGGAATTAACACTGCAGAGATGCCAGCGTGGAGGTCCAGGCTGC 1293  
Qy 1474 TCGAGTTATCAGGAAGTGTCTTCGCTGTTCACTAAGTTTATCAATAGCTTGGTGAAGTCT 1533

Db 1294 TCGGATCATCCGGAACACTACAGCCTTATTTACGCCAGTTTGTCTAGTGGAAACAA----- 1347  
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Db 1348 -----TCGCAAGCTGCCCCCATCACCTCGCTATAGAAAGTTCCTTGCA 1392  
Qy 1594 GTGTCTTTGAAGATCTCAACCAACTACTTCGCACAGCCCCGATGAGGATATGGAACACGAAGA 1653  
Db 1393 GACCTTACAGGACTTGTATCGCTACTTTCAGCCCCCAGAGGAGGAGATGCGCATGAAGA 1452  
Qy 1654 AAAGCAAAACAAATTCGCGCCCTCCGAAACCGTTCAGGACCTGTTCCAAAGGAGGAGAT 1713  
Db 1453 CAAGCAGAACAAAGCTCGCTCACTCAAAAACAGACAAAAATCTTTTCAAGGAAGAGGAAT 1512  
Qy 1714 ACTGAACCTGATCCTCGAAGCTATAGACAAGATCAAGCTCGTACGTCCTCCAGGGGTTCTCT 1773  
Db 1513 GTTGGCCCTTGTCTTAAATTTGCAATTTGACCCGCTTAAATGTCTACAATAGCGTAGCACACTT 1572  
Qy 1774 GGCTGGATTCTCGCGGGAGACGAATCTGACAGAGCTGGGAATGATATCTGGATATTT 1833  
Db 1573 TGCAGGA-----TTGCAAGGGAAGAGATGGCATGGCTTGGAAAGAAATTTCTGAACCTCT 1629  
Qy 1834 GTATCAGTTGCTGGCGCAATATAAAGGCAACACACAGAACTGCGCGCAAGTTCCGGAA 1893  
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Qy 1894 CTGAAACGGTTCACTGGCTGTTCTCGGCTCGGCTCGCAGGCTCGGCGGAGGGCAC 1953  
Db 1684 CTCAATTAACCTTGATTTGGCTCATCAGTAAATTTGGAAGACTAGAAATCTTCTCT-----C 1737  
Qy 1954 CGGCATCTCGACGTGCTGCATCTCATCTGCACTCGCTCGCTGCAAGCGCTCAATATGAT 2013  
Db 1738 AGGTATCTTGAAGTTTTCATCTGATCTTAACTGAAAGCCAGAAAGCTTAAATCTGAT 1797  
Qy 2014 GAGGAGCAACACATAAAAGTGAATATCTCTATTAGAAAAGCAAGCAAGCGGACCCCTAA 2073  
Db 1798 AGCGAGGGCCACATCAAGTCGATCATCTCTCTTTGGATAAGCAAGCGCGGGAATCACA 1857  
Qy 2074 AGTACTAGATGCTATGTTCACTCTGGTGGTAAAGCGCTCGCGTCCGCTCGTCAACA 2133  
Db 1858 GGTTCTGGATATCTGCTGCTCTCTCTGCAATGGGGTTGCAAGTGGAGCAACCA 1917  
Qy 2134 GAACCAATCTGCGACATTTTGTGCGCGCAAGAACTGTTGTGCAAACTGGCTTGT 2193  
Db 1918 GAATCTGATCTGACAACTTGTGCTGCGCGGAGAACTTCTCTGCGACACGACTGAT 1977  
Qy 2194 AGATCAGTATCTAGTGTCCGTCCGAAACATCTTCTGGCGCGAGTAGAAGGGTCCGAGT 2253  
Db 1978 TAAAGATGTAACAGTATCCGGCCAAACATCTTCTGGGAGTCCGGAGGCTCAGCCCA 2037  
Qy 2254 GTACCGCAAAATGGTACTTTCGAGGTGACTATGGACCACTATAGAGAAGACC---ACACATAT 2310  
Db 2038 GTACAAGAAAGTGTACTTTCGAGCTGATTAACAGCAGGTGGAACCCCTTCTTAACAGCAGA 2097  
Qy 2311 GATGCCATCTACGATAGGATGGGTAAACACTACTGTTTATGTCTCCATACCCGGGTGG 2370  
Db 2098 GCCCACATCTCGGGTGGCTGGGCTCTTCTTTCAGGCTATGCCCATACCCAGGAGG 2157  
Qy 2371 TGGTGAAGATGGGGAGGTAAAGCGCTGGGAGACGACTGTACTCGTACGGGTTGATGG 2430  
Db 2158 TGGAGAGGATGGGGAGGCAATGGTGTGGTGAAGCCTGTACTCTATGGCTTTGATGG 2217  
Qy 2431 CGCTACTCTGTGCTCGGCGGAGGAGACCCCGTCAATAGGACTCATCTGGAAGAGCC 2490  
Db 2218 ACTTCACTTGTGTCAGGCCGATACCCAGAGCTGT-----GGCTTCCATCAACAGCA 2271  
Qy 2491 TTATATTAGGAAGTGAAGTGTGATAGGTGTGTGCAATTTGGACTGACGGTACCCCATCATCAA 2550  
Db 2272 CCTCTGAGATCGGATGACGTGATGCTGCTGCTGCACTCGGGGTGCCAGCATCTC 2331  
Qy 2551 CTTCATGTTCAACGGAGTGGGGTGAAGGGATCTCTTCAACCACTTCAATCTGGAAGGAT 2610  
Db 2332 ATTCCGATCAATGGGACCGCTGACGGGATGTTTGAAGAACTTTCAACACAGACGGCT 2391

Qy	2611	GTTCCTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCTCTGCTGGGCGGAGA	2670
Db	2392	CTTCTTCCTCTGTGATGAGCTTTTCAGCAGGTGTCAAAGTAGCTTTCTGATGGGTGGACG	2451
Qy	2671	ACACGGTAGACTCCGGTACCGGCTCCAGAAAGGCTACTCCCGCGTGGTGAGTCTCTCTCT	2730
Db	2452	TCATGGAGAGTTAAAGTTCTGCTCCTCTGGCTATGCCCTTGCTGCTATGAAGCCTTACT	2511
Qy	2731	GGCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTCGGGCAA CCTGTC-----CAA	2784
Db	2512	TCCAAAAGAGAAGATGAGATTGGAGCCTGTCAAAGAAATATAAAACGTGATCTGATGGCAT	2571
Qy	2785	GGCGGCTTGCGTGGACCCCGCTAGTACAGGACGATACGGCTTTTGTGCTCTACGCTGT	2844
Db	2572	TAGAGATCTCTTGGGTACCAACCCAGTTCTCTCTCCAAAGCCTCTTTTCAATCCATGCCCGT	2631
Qy	2845	TGATACTTTACAGATTACTCTGCGCTACATATGTGGAA CAAATCAGAGACAAGCTAGCTGA	2904
Db	2632	AGACACAGTCAGTTATTTTGGCACCTCACCTAGAAAGATCCGAGACAGACTAGCTGA	2691
Qy	2905	AAATATTCAAGAAATGTGGGCTATGAATAAGATCGAAGAGAGGTGGAATGTACGGCGACCA	2964
Db	2692	AAACATCCATGAGCTTTGGGGAATGAATAAAATAGAACTTTGGCTGGACTTTTCGGCAGAT	2751
Qy	2965	GAGAGAGACTTGCAACAAGATCCACCCTCGCTCGTCCCTTCGAGCGACTCCCGCCCGC	3024
Db	2752	ACGAGATGCAAAATAAAGACAACACCCTTGCTTGTGGAGTTTCAAAGCTTCCGAGAAAC	2811
Qy	3025	TGAAACAGATACCATATACAACCTGTGTGCAGACACTCAAGACTATCCTGGCTCTGGG	3084
Db	2812	TGAGAGAACTATAACCTGCAATGTCAACTGAACACCTTAAACCCCTTTGGCCCTGGG	2871
Qy	3085	CTACTACATCAGCTTTAGATAAGC---CTCCAGCAGCGCATCCGCAACGTTCTGTCGCCAA	3141
Db	2872	GTGCCAATTGCTCTCATGTTAAACCAGCTGCTGAGGAGGATCTCAAGAAAGTCAAACTGCC	2931
Qy	3142	TGAACCTTTCAATGCAAGTCCAAAGCGGTACAAGCAGACACCACTGCACTGAGTGTCTGTCAC	3201
Db	2932	CAAAAACATATATGATGTCCAAAGCGCTATAAGCCAGCCCTTTGGATTTGTCTGATGTGAA	2991
Qy	3202	CCTGACACCCNAGATGGATGAGCTAGTAGCCAGCTGGCTGAGAACACCCACACACCTTG	3261
Db	2992	GCTGTTACCTCTCAAGAAATTTTGTAGTGAATAAGCTTGCAGAAATGCACAAATGTTTG	3051
Qy	3262	GGCCAGGGAGAGGATACAGCAGGATGGACTTTACGGACTTAATCAGGACTCGGACATGCA	3321
Db	3052	GGCAAAAGACAAATAAACAAGATGGACCTATGGCATCCACAGAGTTTGAGACAA	3111
Qy	3322	TCGATCCCCGCACCTGTGTCCATACCCGAAAGTTTGACGATGCCATCAAGAAGGCCAACAG	3381
Db	3112	AAGAAATCCCGCTCTGGTGCCATATGCATTACTGGATGAGCGTACCAAGAAGTCAAAACAG	3171
Qy	3382	GGACACAGCCTCGAGACTGTGAGAACCTCTCTGGTCTACGGGTATATGCTGGAACCCGCC	3441
Db	3172	GGACAGCCTGCGGGAAAGCTGTGCGCACTTTTGTGTGGTTACGGGTATAACATTTGAGCCATC	3231
Qy	3442	TACTGGGGAGCAGCATGAGACACTCTGTTTGGAAAGCTCAAAAAGAGCAAGCCGACTT	3501
Db	3232	-----AGACCAAGAACTAGCTGACTCGGCTGTGGAGAGGTCTAGCATAGACAAGAT	3282
Qy	3502	CAGAACATACCGCGCTGAGAAGAACTATGCCGTCAAGCTCTCGGAAAGTGGTACTTTGAGATT	3561
Db	3283	CCGATTTTTCGGGTAGAGCGATCTTATGCAATGAGATCTGGAAGTGTATTTTTGATT	3342
Qy	3562	TGAGATCTTAACGGCTGGACCTATGAGGGTCCGGCTGGGCTCACGCTGATATGGACCAGG	3621
Db	3343	TGAAGTGTGACTGGAGGAGACATGCGAGTCCGGCTGGSCGAGGCCAGCTCTGCACCTGA	3402
Qy	3622	AATGATGCTCGGAACAAGACGAGAACTCTCTGGGCTTTTGATGGTTTACAAATGAGGAAAAAGT	3681
Db	3403	TGTGAGCTGGGGCCGATGACCAAGCCTTTGTGTTTGAAGGCAACAGGGCCACGCGTTG	3462

QY	3682	GTACAGCGGTAA	CAC	TGAGTCTTT	TCG	CAGCAAG	CAATGGG	CTGTTGGT	CA	CGTACAGT	CGGGGT	3747
DB	3463	GCATCAAGGAAG	---	TGGG	TATTTT	TGGG	GGTG	CACTGGC	AGCCAGGGG	ATGTG	TGCGATG	3519
QY	3742	GTTCCTAGATCT	CA	TTCATTAAG	ACGATAAGT	TTCTCACTCA	ACGCGTGAG	TTGTTGAT	TGGA	3801		
DB	3520	TATGATTAAC	CT	TGATGAT	CTCTCA	TGATCTT	CACACTGA	ATGGG	AGCTGCTGAT	CAAC	3579	
QY	3802	TGCTCTTTGGG	GGAGAG	CTAC	GTTTGCTG	TGATGTCC	AGGGTGACAA	---	CTTTGTAC	CTGC	3858	
DB	3580	CAACAAAGGCT	CTGAA	CTTGCTTC	GTGATCA	CGAGATTG	GAGAA	TGGCTTC	TGTCGCCAT	3639		
QY	3859	TTGCACGCTT	GGTGTTC	GGCCAA	AAAGCCAG	GTGTAA	CATACGGT	CAGGAC	GTGAACAC	CGCT	3918	
DB	3640	CTGCTGTCT	GGGTCT	TATCT	CAGATCG	CCCGCATG	AATCTCGG	ACAGATGCC	AGTACCTT	3699		
QY	3919	GAATACTCT	CAACAT	GTGCTG	CAAGGAGG	ATATGA	ACCATTC	TGCTGTCA	ATATGA	3978		
DB	3700	CAAGTTTTAT	ACCATGTG	CGGTCTCC	AAAGAGG	GGCTTTG	AGCCCTTT	TGCTGTCA	ACATGA	3759		
QY	3979	GAGAGCTG	ACTCACTGG	TATACCA	AAAGAC	CCCGCATCTT	CGAGAA	TACGGATG	AGAT	4038		
DB	3760	CAGAGATG	TGTCTATG	TGGTTC	AGCAAG	CGCCTCC	CGACGTT	TGTCAA	---	CGTGCCAA	3816	
QY	4039	GATCGAC	CAACAGATAG	ATGTGAC	CCGATAC	CAACAGCTGG	TTTCAGAT	ACACCTCC	ATGCCT	4098		
DB	3817	GGATATCC	ACACATAG	AGGTCTAT	GAGATG	TATGGC	ACCATGG	ACAGCCCT	CCGTCTCT	3876		
QY	4099	CAAGATTTCC	ACAACAG	CTTTTG	AGACGAT	TGGAGA	4133					
DB	3877	CAAGGTG	ACGATTAAGA	CATTTG	GCACAC	AGAATA	3911					

## RESULT 2

```

US-11-266-748A-31954
; Sequence 31954, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/6662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31954
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-31954

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Query Match 1.3%; Score 63; DB 8; Length 1406;  
Best Local Similarity 70.6%; Pred. No. 3.4e-08;  
Matches 84; Conservative 0; Mismatches 35; Indels 0; Gaps 0;



Qy 675 CCCAGGTGAAGCTGCTGGTGGACCTCGCATCTCCAGCAACACAGATCCGAGGCG 734  
Db 789 CCATAGGAGAGGCTTGCTGGTGGACCTCGCATCTCCAGCAACACAGATCCGAGGCTGAAGGAG 848  
Qy 735 AGAAGGTGCGAGTCGGAGATGACTTGAATTCAGTCTCGTGGCCATTGAGAGATCTTG 793  
Db 849 AAAAGTCCGGTTGGGGATGACATCATCTTGTAGTGTCTCTCCGAGGCTACCTG 907

## RESULT 3

US-11-266-748A-377158/c  
; Sequence 377158, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 377158  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-11-266-748A-377158

Query Match 1.1%; Score 54.8; DB 8; Length 583;  
Best Local Similarity 65.6%; Pred. No. 6.8e-06;  
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 3162 ACGGCTACAAGCCAGCACCCTCGACCTGAGTGTGTACCCCTGACACCCCAAGATGGATG 3221  
Db 455 AAGGCTACAACCTCAGCCCCCGACCTTAGTGTGTACCTGTCCCGGAGCTGCAGG 396  
Qy 3222 AGCTAGTAGGCGAGCTGCTGAGAACACCCCAACCTTTGGCCGAGGAGGATACAGC 3281  
Db 395 CCATGGCAGAACAACTGGCGAATAATTACCAACACCTGGGGCGGAAGAAGCAGG 336  
Qy 3282 AG 3283  
Db 335 AG 334

## RESULT 4

US-11-266-748A-460537  
; Sequence 460537, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 460537  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-11-266-748A-460537

Query Match 1.1%; Score 54.8; DB 8; Length 583;  
Best Local Similarity 65.6%; Pred. No. 6.8e-06;  
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 3162 ACGGCTACAAGCCAGCACCCTCGACCTGAGTGTGTACCCCTGACACCCCAAGATGGATG 3221  
Db 129 AAGGCTACAACCTCAGCCCCCGACCTTAGTGTGTACCTGTCCCGGAGCTGCAGG 188  
Qy 3222 AGCTAGTAGGCGAGCTGCTGAGAACACCCCAACCTTTGGCCGAGGAGGATACAGC 3281  
Db 189 CCATGGCAGAACAACTGGCGAATAATTACCAACACCTGGGGCGGAAGAAGCAGG 248  
Qy 3282 AG 3283  
Db 249 AG 250

## RESULT 5

US-11-266-748A-373619  
; Sequence 373619, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293





APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nickolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
TITLE OF INVENTION: Polypeptides Encoded Thereby  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
PRIOR FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 14642  
LENGTH: 838  
TYPE: DNA  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq. ID no. 12468112  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: as cited in SEQ ID NO 59527  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 12615972  
OTHER INFORMATION: as cited in SEQ ID NO 62455  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 13596229  
OTHER INFORMATION: as cited in SEQ ID NO 68800  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(838)  
OTHER INFORMATION: Ortholog of Ceres Seq ID NO 15179393  
OTHER INFORMATION: as cited in SEQ ID NO 0  
US-11-056-355B-14642

Query Match 0.8%; Score 39.6; DB 9; Length 838;  
Best Local Similarity 49.5%; Pred. No. 0.46;  
Matches 102; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 2580 GATCCTTACCAACTTCAATCTGGAAGGCATGTTCTTCCCGTCAATCAGCTGCTCTAGTA 2639  
DB 179 GGTCCATCTACCAACAGATTGCGAGCCATGCTGAACCTGATCATCATCGCGCCATCA 238  
QY 2640 AGCTGAGTTGCTGGTTCCTGCTGGCGGAGAACACGCTAGACTCGGTACGCGGCTCCAG 2699  
DB 239 ACTTGGCTCGGGATCTCCGCGACGTTGACAACTTCGCGACATCGCGGGTTCCGCA 298  
QY 2700 AAGGCTACTCCCGCTGGTGGAGTCTCTCCGCGCAGAGATCTCAGCCTGGAGCCGT 2759  
DB 299 CAGGCTTCTCTCGGCTTCGTGCTGCTGATCCAGCCAGTTCGGGTGGCTGGAGCAGC 358  
QY 2760 GCTTCTACTTCGGCAACCTGTCAG 2785  
DB 359 CCTTCGGTCCCAAGACCAAGTCCAG 384

RESULT 9  
US-11-218-305-1911  
Sequence 1911, Application US/11218305  
Publication No. US2006014195A1  
GENERAL INFORMATION:  
APPLICANT: MONSANTO TECHNOLOGY, LLC  
APPLICANT: McLaird, Paul L.  
APPLICANT: Tao, Nengbing  
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
TITLE OF INVENTION: Corn.  
FILE REFERENCE: 38-21 (53660)B

CURRENT APPLICATION NUMBER: US/11/218,305  
CURRENT FILING DATE: 2005-09-01  
PRIOR APPLICATION NUMBER: US 60/606,880  
PRIOR FILING DATE: 2004-09-01  
NUMBER OF SEQ ID NOS: 25043  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1911  
LENGTH: 4017  
TYPE: DNA  
ORGANISM: Zea mays  
US-11-218-305-1911

Query Match 0.8%; Score 39.6; DB 9; Length 4017;  
Best Local Similarity 49.5%; Pred. No. 1.3;  
Matches 102; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 2580 GATCCTTACCAACTTCAATCTGGAAGGCATGTTCTTCCCGTCAATCAGCTGCTCTAGTA 2639  
DB 3340 GGTCCATCTACCAACAGATTGCGAGCCATGCTGAACCTGATCATCATCGCGCCATCA 3399  
QY 2640 AGCTGAGTTGCTGGTTCCTGCTGGCGGAGAACACGCTAGACTCGGTACGCGGCTCCAG 2699  
DB 3400 ACTTGGCTCGGGATCTCCGCGACGTTGACAACTTCGCGACATCGCGGGTTCCGCA 3459  
QY 2700 AAGGCTACTCCCGCTGGTGGAGTCTCTCCGCGCAGAGATCTCAGCCTGGAGCCGT 2759  
DB 3460 CAGGCTTCTCTCGGCTTCGTGCTGATCCAGCCAGTTCGGGTGGCTGGAGCAGC 3519  
QY 2760 GCTTCTACTTCGGCAACCTGTCAG 2785  
DB 3520 CCTTCGGTCCCAAGACCAAGTCCAG 3545

RESULT 10  
US-11-174-307B-4053  
Sequence 4053, Application US/11174307B  
Publication No. US20060143729A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nickolai  
APPLICANT: BROVER, Vyacheslav  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS  
FILE REFERENCE: 2750-1601PUS2  
CURRENT APPLICATION NUMBER: US/11/174,307B  
CURRENT FILING DATE: 2005-06-30  
PRIOR APPLICATION NUMBER: 60/583,671  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/583,781  
PRIOR FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/583,651  
PRIOR FILING DATE: 2004-06-30  
NUMBER OF SEQ ID NOS: 5544  
SEQ ID NO 4053  
LENGTH: 1189  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1189)  
OTHER INFORMATION: Ceres cdna ID no. 21666056  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1189)  
OTHER INFORMATION: Ceres CLONE ID no. 1277411  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1189)  
OTHER INFORMATION: Also known as Ceres CDNA ID no. 24358413  
US-11-174-307B-4053

Query Match 0.8%; Score 39.2; DB 9; Length 1189;  
Best Local Similarity 56.1%; Pred. No. 0.77;  
Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;



Db 303 ATCTACTCGCTCGTGGCTCGCTCGGGGGCGGCGGACGTCGCGACTGGCTCGGCGGCGG 362  
Qy 1973 CACTGCATCCTCATCGACTCGCC 1995  
Db 363 TACACCATGGTGTCTCGCGGCGG 385

RESULT 14

US-11-218-305-12750  
; Sequence 12750, Application US/11218305  
; Publication No. US2006014195A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE OF INVENTION: Corn.  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12750  
; LENGTH: 1847  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-218-305-12750

Query Match 0.8%; Score 39; DB 9; Length 1847;

Best Local Similarity 54.5%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;  
Matches 78; Conservative 0;

Qy 1853 ATATAAAGGCAACACACAGAACTCGCGCGAGTTCGCGAAGTTCGGAACCTCGAACCGGTTCAACTGG 1912  
Db 228 ATGACGAGGACCTCAAGATCACGGACACGACATCGAGATCTCTCGCGGCATCATCAAT 287  
Qy 1913 CTGTTCTCGGCGCTCGGCTCGAGGCTCGGGGAGGACCGGATGCTCGACGTGCTG 1972  
Db 288 ATCTACTCGCTCGGCTCGCTCGGCGGCGGCGGCGGACGTCGCGACTGGCTCGGCGGCGG 347  
Qy 1973 CACTGCATCCTCATCGACTCGCC 1995  
Db 348 TACACCATGGTGTCTCGCGGCGG 370

RESULT 15

US-11-292-078-9801  
; Sequence 9801, Application US/11292078  
; Publication No. US20060195941A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517,346 - 38-21(52274)C  
; CURRENT APPLICATION NUMBER: US/11/292,078  
; CURRENT FILING DATE: 2005-12-02  
; PRIOR APPLICATION NUMBER: US 10/021,323  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,619  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 9801  
; LENGTH: 604  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:

; NAME/KEY: unsure  
; LOCATION: (1)..(604)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3828-028-Q6-K6-C7  
US-11-292-078-9801  
  
Query Match 0.8%; Score 38.8; DB 7; Length 604;  
Best Local Similarity 58.8%; Pred. No. 0.65;  
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
  
Qy 1346 AAGTCTTACGAAACGAAGAAAGCGGTGGGTAAAGTAGAAGAGCAAGCGATTCTC 1405  
Db 369 AAGTTTGAAGAGCAAACTAGAGAGAGGTTAAAGTTGAAGAGCAGGATGTGCTTCAG 428  
Qy 1406 CACGAGGAGGCAAGATGGACGATGGCTTCGACCTCTCCAGGTCAAGAGGAA 1459  
Db 429 CTTAAGAGGAGAGGTTTCAGAAAGACCTCGAGATTTCTAGGCTAAAGAGGAA 482  
  
Search completed: October 11, 2006, 02:43:59  
Job time : 1555 secs



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